Run

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
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2802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             February 18, 2001, 19:19:51; Search time 3075.67 Seconds (without alignments) 6383.969 Million cell updates/sec
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1117: em_estpl6:*
1120: em_estpl8:*
1210: em_estr014:*
1221: em_estr015:*
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1232: em_estr017:*
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1255: em_estr018:*
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190: 191: 192: 193:	
gb_gss25:* gb_gss26:* gb_gss27:* gb_gss28:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20 20 20 20 20 20 20 20 20 20 20 20 20 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result No.
94 88.888.6888.6888.6888.6888.6888.6888.6	101.2 100.8 99.2 99.9 97.6 97.6	0. 20	. 44 6 0 0 0 0 0	Score
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	679391 1238397 1393915 1024672 164990 164990 164990 164990	AW011114 AW108557 AW158294 AW158294 AW107536 AI768053 BE573696 AW012320 AW012320 AW012320 AW046425 AM1046425	69651714 6651714 9699679 94132 248626 746915 746915 77370 77370 77370 77370	
BE877; BE3900 BE7914 AW50543 AW50543 AM50543 AM50543 AM509366 BE3905 AA570930 AA570936 BE3856 BE3856 AM570157 AM60996 AM21124058 AM231333	AA10796 AA26793 AI33383 AJ39399 AI0246 AA26499 BE266 BE410 BE275	2000278788	N941 1248 1746 1746 1746 1746 1746 1746	Descrip
101 60148 142 60158 144 60158 150 UI-HF-1 150 ba72hh 150 ba72	1 mp04d08. 91 z129a02. 97 GH14435. 15 AJ39391. 72 ov60h04. 0 LD08686. 0 LD08686. 478 601192.	57 & hd22ac 57 & hv1085 94 za39ec 36 u191ac 596 60133 596 60133 20 um07d0 99 uc85h0 2 mx86560 2 mx86560	14 AV6517 79 zi78c0 2 za25g06 26 qh77b1 15 ul09a1 11 za25g06 11 za25g06 11 da94c0 11 da94c0	tion
115 97 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2015. F		126	

ALIGNMENTS

RESULT 1
AV651714 638 bp mRNA EST 07-SEP-2000
DEFINITION AV651714 GLC Homo sapiens cDNA clone GLCCSG03 3', mRNA sequence.
ACCESSION AV651714:
VERSION AV651714: 61:9872728
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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JOURNAL COMMENT
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Best Local Similarity 89.5
Thes 619; Conservative
2338 tgaaggttcccgaggacatgagtctgtaggagcaagggcacaaactgcagctgtgagtgc 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1918
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                                                                  aaaacaaacagaaacaacaaatttggatcaaaaggagaaaatgataagtgacaaaagc 2277
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                                                                                                          AAAACAAACAG-AACACAAATTTGGATCAAAAGGAG-AAATGATAAGTGAC----- 472
                                                                                                                                                                                 TGTGGGGTATACAGCATTGACTCAGATATAGATCCTGAGCTCACAGAGTTTATAGTTGAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
201203, P. R. China
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201203, P. R. China
Tel: 86-21-50801919(ex.45)
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ammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 638)
                                        160
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clone is available at CHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tlssue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="GLCCSG03"
/clone_lib="GLC"
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Pred. No. 1.2e-110;
0; Mismatches 18;
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                   Query Match
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Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washd-NCI human EST project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA699679 461 bp mRNA EST 19-DEC-19
z178c07.sl Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens
clone_IMAGE:446892 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cione is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -4,0ml3 fwd. Er from Amersham High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314.286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                  constructed by Bento Soares and M.Fatima Bonaldo."
126 c 86 g 131 t
                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
/db_xref-"GDB:1351149"
/db_xref-"taxon:9606"
/clone-"IMAGE:446892"
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                15.9%;
99.1%;
Score 445.2; DB 10;
Pred. No. 1.3e-92;
0; Mismatches 3;
                                Length
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N94132 454 bp mRNA EST 05-APR-1996 za25g06.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE: 293626 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.linl.gov)
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
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/sex="male" 20 week-post conception fetus"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="TOH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT7T3D (
                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3801473"
/db_xref="taxon:9606"
/clone="IMAGE:293626"
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                                                                                                                                                                                                                                            /clone_lib="Soares fetal liver spleen lNFLS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTGTCTCTGCATCCATTTGAACACATTATTAAGCACCGATAATAGGTAGCCTGCTGTG
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                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Email: Robert_Strausberg@nlh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 608 Std Error: 0.00
Seg primer: -400F from Gibco
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Verto
Mammalia; Eutharia; Primates; Catarrhini; Hor
1 (bases 1 to 343)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap;
                                                                                                                                                                                                                                                                                                                                                                                                     (HUMAN); mRNA sequence.
AI248626
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                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                            Tumor Gene Index
                                                                                                                                                                                                                National Cancer Institute, Cancer Genome
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quality sequence stop: 338.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

a 120 c 100 g 118 t
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Pred. No. 7.4e-86;
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                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches 340; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggaagtcggaggtccccaaatctgccgtgtatgtggggacaaggccactggctatcactt 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctttgtacactgtgaggacacagagtctgttcctggaaagcccagtgtcaacgcagatga 274
                                                                                                                                                                                                                                                                                                                                         GTGCCAGGCCTGCGCCTGCGCAAGTGCCTGGAGAGCGGC 1
                                                                                                                                                                                                                                                                                                                                                     gtgccaggcctgccctgcgcaagtgcctggagagcggc 494
                                                                                                                                                                                                                                                                                                                                                                                                 CCGGCTGAGGTGCCCCTTCCGGAAGGGCGCCTGCGAGATCACCCGGAAGACCCGGCGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAATGTCATGACATGTGAAGGATGCAAGGGCTTTTTCAGGAGGGCCATGAAACGCAACGC
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          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 794)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson R.
The WashU-RCI Mouse EST Project 1999
                                                                                                                                                                                                                                  AI746915 794 bp mRNA EST 22-JUN-1999 ul09a10.yl Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2076282 5' similar to TR:054915 054915 PREGNANE X RECEPTOR.
Unpublished (1999)
                                                                                                                                                               house mouse.
                                                                                                                                                                                          AI746915.1 GI:5125179
                                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; Score 340; DB 18; llarity 100.0%; Pred. No. 2.8e-68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="InAGE:1850687"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/dev_stage="20_week-post_conception_fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain-"C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%;
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139 agttggcttcaaaccatccaagaggcccagaagcaaacctggaggtgaggacccaaagaaa 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 --- TCAACGTAGAGGAAGATGGAGGTCTTCAAATCTGCCGTGTATGTGGGGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgtcaacgcagatgaggaagtcggaggtccccaaatctgccgtgtatgtggggacaagg
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                                 agaaaagtgaacggacaggggactcagccactgggagtgcagggggctgacagaggagcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGAGCCGAGTTGGCCTTGTACAGTGTGAAGAAGCAGACTCTGCCTTGGAAGAGCCCCA 411
                                                                                                                                           agaaggagatgatcatgtccgacgaggccgtggaggagaggcgggccttgatcaagcgga 558
                                                                                                                                                                                                                                                                  ggaagacccggcgacagtgccaggcctgccgcctgcgcaagtgcctggagagcggcatga
                                                                                                                                                                                                                                                                                                                                                                                   AGAAGAGGGAANAGATTGAGGCTCCACCGCCTGGGAGGCANGNGCTGACGGAAGAACAGC
                                                                                                                   AGAAAGAGATGATCATGTCCGATGCCGCTGTGGAGCAGAGGCGGCCTTGATCAAGAGGA
                                                                                                                                                                                                                                 GGAAGACACGACGCCAGTGCCAGGCCTGCCGTTTTGCGCAAGTGCCTGGAGAGTGGCATGA
                                                                                                                                                                                                                                                                                                                                                    CCATGAAACGCAATGTCCGGCTGAGGTGCCCCTTCCGCAAGGGGAACCTGCGAGATCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: custom primer used High quality sequence stop: 472.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Index vector: pME18S-FL3; Site_1: Drail (CACTGTGTG);
Site_2: Drail (CACCATCTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT];
double-stranded cDNA was igated to a Drail adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct Drail
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
'(University of Tokyo Institute of Medical Science).
'Custom primers for sequencing: 5' end primer
CCTCTGCTCTAAAAGCTGCG and 3' end primer
CCACCTGCAGCTCGAGCACA."

2 other
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/dev_stage="embryo, 14 dpc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 338.2; DB 24; Length 794; Pred. No. 8.7e-68; O; Mismatches 96; Indels 3;
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VERSION
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Best Local
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                                                                                                         2310
                                                                                                                                                          2251 aaggagaaaatgataagtgacaaaagc-agcacaaggaatttccctgtgtggatgctgag 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
365 AAAGGAGAAATGATAAGTGACAAAAGCNACCACAAGGAATTTCCCTGTGTGGATGCTGAG 306
                 ct9t9at9gcaggcactgggtacccaagtgaaggttccccgaggacatgagtctgtaggag 2369
                                                                    CTGTGATGGCGGGCACTGGGTACCCAAGTGAAGGTTCCCGAGGACATGAGTCTGTAGGAG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggatgatgatcagggagctgatggac 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCGCTGATCCCAGAGCTGATGGAC 794
                                                                                                                                                                                                              352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.lln1 Seq primer: m13 -40 forward High quality sequence stop: 279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

This clone is available royalty-free through LLNL; contact the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 365)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N69311 365 bp mRNA EST 13-MAR-1996 za25906.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:293626 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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314 286 1810
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:3801473"
/db_xref="taxon:9606"
/clone="IMAGE:293626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares fetal liver spleen lNFLS"
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                                                                                                                                                                                                                         Score 335; DB 143
Pred. No. 4.1e-67;
                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                           Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 472)

Marra, M.; Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S.; Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising B. weller T. the Corner of Corner Bullon D. and Theising B.
                                                                                                                                                                                                                                                                                                                                                                                                                 vector to vector length is 506 Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
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The WashU-HHMI Mouse EST Project
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                                                                             double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library
                                         Bonaldo."
                                                                                                                                               constructed and normalized by
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/clone="IMAGE:737758"
/clone_lib="Soares mouse NML"
/tissue_type="liver"
                                                                                                                                                                                                                                      /lab_host="DH10B"
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                    141 c
                  115 g
                    105 t
                                                             Bento Soares
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                    2 others
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                                                                                                                                                                                                                                                                                                                                                                            l (bases 1 to 493)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Glibons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
                                                                                                                                                                                                                               Contact: Sandy Clifton, Ph.D. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Other_ESTs: da94c06.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AW871811
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                                                                                                                                                     Library constructed by B. Korn PhD. and S. Henze DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus Laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      African clawed frog
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                                                                                                                through the RessourcenZentrumPrimarDatenbank, Berlin, address: www.rzpd.de)
                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
                                                                                              primer: -40RP from Gibco
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                                                      quality sequence stop: 4
                                    1. .493
/organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tatcacttcaatgtcatgacatgtgaaggatgcaagggcttttttcaggaggggccatgaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    aatttccggc.696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gaacggacagggactcagccactgggagtgcaggggctgacagaggagcaggatgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cggcgacagtgccaggcctgccgcctgcgcaagtgcctggagagcggcatgaagaaggag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCACTCAACTGGTTGGGGCCCACACCAAAACCTTTGACTTCAACTTCACCTTCTCCAAG
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                                                                                                                                                                                                                                                          AA679591 200 bp mRNA EST 19-DEC-1997 zj49d12.sl Soares_fetal_liver_spleen_lNFLS_Sl Homo sapiens cDNA clone IMAGE:453623 3' similar to TR:6410518 G410518 ORPHAN NUCLEAR RECEPTOR:OF STEROID/THYROID SUPERFAMILY. ;, mRNA sequence.

AA679591
Eukaryotá; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 200)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-KCI human EST project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                             AA679591.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="whole tadpole"
/dev_stage="stage 24"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Xenopus laevis tadpole stage
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:"
                                                                                                                                                                                                                                             GI:2660113
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RESULT 10
AW511148/c
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                                                                            REFERENCE
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                                       TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aacgcccggctgaggtgccccttccggaagggcgcctgcgagatcaccccggaaagacccgg 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTTCAATGTCATGACATGTGAAGGATGCAAGGGCTTTTTCAGGAGGGTTATGAAACGC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cacttcaatgtcatgacatgtgaaggatgcaagggctttttcaggagggccatgaaacgc 389
                                                                                                                                                                                                                                                                                                                                                                                                CGACAGTGTCCAGGC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                      cgacagtgccaggcc 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGAGGAAGTCGGAGGTCCCCAAATCTGCCGTGTATGTGGGGACAAGGCCACTGGCTAT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGCCCGGCTGAGGTGCCCCTTCCGGAAGGGCGCCTGCGAGATCACCCGGAAGACCCGG
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  AW511148 463 bp mRNA EST 03-M hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 075469 ORPHAN
              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                    Homo sapiens
                                                                                                                                                           numan
                                                                                                                                                                                                AW511148.1 GI:7149226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                 RECEPTOR PXR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                          (bases 1 to 463)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:453623"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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96.9%;
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Pred. No. 1.6e-32;
0; Mismatches 6;
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SOURCE
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                                                                                                                                                                                                AUTHORS
TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 ggcttttcagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 GTTCCTGGAAAGCCCAGTGTCAACGCAGATGAGGAAGTCGGAGGTCCCCAAATCTGCCGT 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 GTGAGACCAAAGGAAAGCTGGAACCATGCTGACTTTGTACACGTGAGGACACAGAGTTCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 gtgagacccaaagaaagctggaaccatgctgactttgtacactgtgaggacacagagtct 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtatgtggggacaaggccactggctatcacttcaatgtcatgacatgtgaaggatgcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gttcctggaangcccagtgtcaacgcagatgaggaagtcggaggtccccaaatctgccgt 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176;
          Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe;S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 215)
Carninci; P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                AV108557 215 bp mRNA EST AV108557 Mus musculus liver C57BL/6J 13-day embryo CDNA clone 2510047D01, mRNA sequence.
RIKEN Mouse ESTS
                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                               AV108557.1 GI:5256105
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE: 2910224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374
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91.7%;
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Best Local Similarity 85.68;
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                                                                                                                                                                                                                                                                                                                                                                                                            181 ATGCCGCTGTGGAGCAGAGGCGGGCCTTGATCAAG 215
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      Expressed sequence tags from Xenopus Unpublished (1999)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                  Xenopodinae; Xenopus.

1 (bases 1 to 432)

1 (bases 1 to 432)

Schutz, K., de la Bastide, M., Huang, E.N., Nascimento, L., Schutz, K., Vil, M.D. and
                                                                                                                                                                                                                                                                                                   za39e07.x1 Xenopus
5', mRNA sequence.
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                    Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.) 5(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                   African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@rtc.riken.go.jp
                                                                                                                                                                                                                                                                                              mRNA sequence.
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81-298-36-9098
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/clone="2510047D01"
/clone_lib-"Mus musculus liver C57BL/6J 13-day embryo"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                             library Xenopus laevis cDNA clone za39e07
                                                                                                                                                                                                                                                                                                                               mRNA
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Pipidae;
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Contact:
                   Unpublished (1999)
Other_ESTs: u191a06.x1
                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                              AW107536.1 GI:6078336
                                                                                                                                                                                                                                                                         mRNA sequence.
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                                                                                                                                                                                                               nouse mouse.
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   Marra M/WashU-NCI Mouse EST Project 1999
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/dev_stage-"tadpole"
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74.0%;
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267 gcagatgaggaagtcggaggtccccaaatctgccgtgtatgtgggggacaaggccactggc 326
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., "The WashD-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW107536 601 bp mRNA EST 20-OCT-1999 u191a06.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2159410 5' similar to gb:J03258 VITAMIN D3 RECEPTOR (HUMAN); gb:U15548 Mus musculus beta 2 thyroid hormone receptor (MOUSE);,
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 601)
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Plate: za39 row: e column: 07
Seq primer: M13 universal forward primer
High quality sequence stop: 432.
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CDNA synthesis with oligo dT Xba I (Xba I cloning site).

RNA: stage 50-56 tadpoles, total brain tissue, GTC extraction method."
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/clone_lib="Xenopus EST library"
/tissue_type="total brain tissue"
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/db_xref="taxon:8355"
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Pred. No. 7.9e-26;
0; Mismatches 72;
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                                                                                                                           541
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                                                                                                                                                                           648 cagatgaaaacctttgacactaccttctcccatttcaagaatttccggctgcca 701
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                                                                                                                           CACCACAAGACCTACGACCCCACCTATGCCGGGACTTCCGGGACTTGCTGCCTCCA 594
                                                                                                                                                                                                                                                                                                                                                               gtggaggagaggcgttgatcaagcggaagaaaagtgaacggacagggactcagcca 587
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Email: mouseestévatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
AI768052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Norgan: kidney; Vector: pME18S-FL3; Site_1: DralII (CACTGTGTG); Site_2: DralII (CACCATGTG); ist strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DralII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DralII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTGCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCACCACACA."

173 g 119 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B"
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/clone="IMAGE:2159410"
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/strain="C57BL"
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 Mismatches

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     mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 ccccaaatctgccgtgtatgtggggacaaggccactggctatcacttcaatgtcatgaca 347
                                                528 gtggaggagaggcgggccttgatcaagcggaagaaaagtgaacggacagggactcagcca 587
                                                                                                                                       468 cgcctgcgcaaggtgcctggagagcggcatgaaggaggagatgatcatgtccgacgaggcc 527
                                                                                                                                                                                                                                                                                                                         TGTGAAGGCTÇCAAAGGCTTCTTCAGGCGAAGCATGAAGCGGAAGGCACTATTCACCTGC 269
GTGCAGAGGAAGCGGGAGATGATCCTGAAGCGGAAGGAGGAGGAGGACGCCTTGAAGGACAGT 92
                                                                                                        CGGCTCAAACGCTGTGTGGACATCGGCATGATGAAGGAGTTCATTCTGACAGATGAGGAA 152
                                                                                                                                                                                                                 CCCTTC---AACGGGGACTGCCGCATCACCAAGGACAACCGACGCCACTGCCAGGCCTGC 212
                                                                                                                                                                                                                                                              cccttccggaagggcgcctgcgagatcacccggaagacccggcgacagtgccaggcctgc 467
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCGGATCTGTGGGGGTGTGTGGAGACCGAGCCACTGGCTTTCACTTCAATGCTATGACC 329
                                                                                                                                                                                                                                                                                                                                                           wi46b06.xl NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2393267 3' similar to gb:J03258 VITAMIN D3 RECEPTOR (HUMAN);, mRNA sequence. aI768052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-GAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.ilnl.gov/Dbrp/image/image.html
Insert Length: 996 Std Error: 0.00
Seq primer: -400P from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-*Organ: colon; Vector: pT773D-Pac (Pharmacia) with a /note-*Organ: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Colo was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1143551).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143.8;
Pred. No. 8.0
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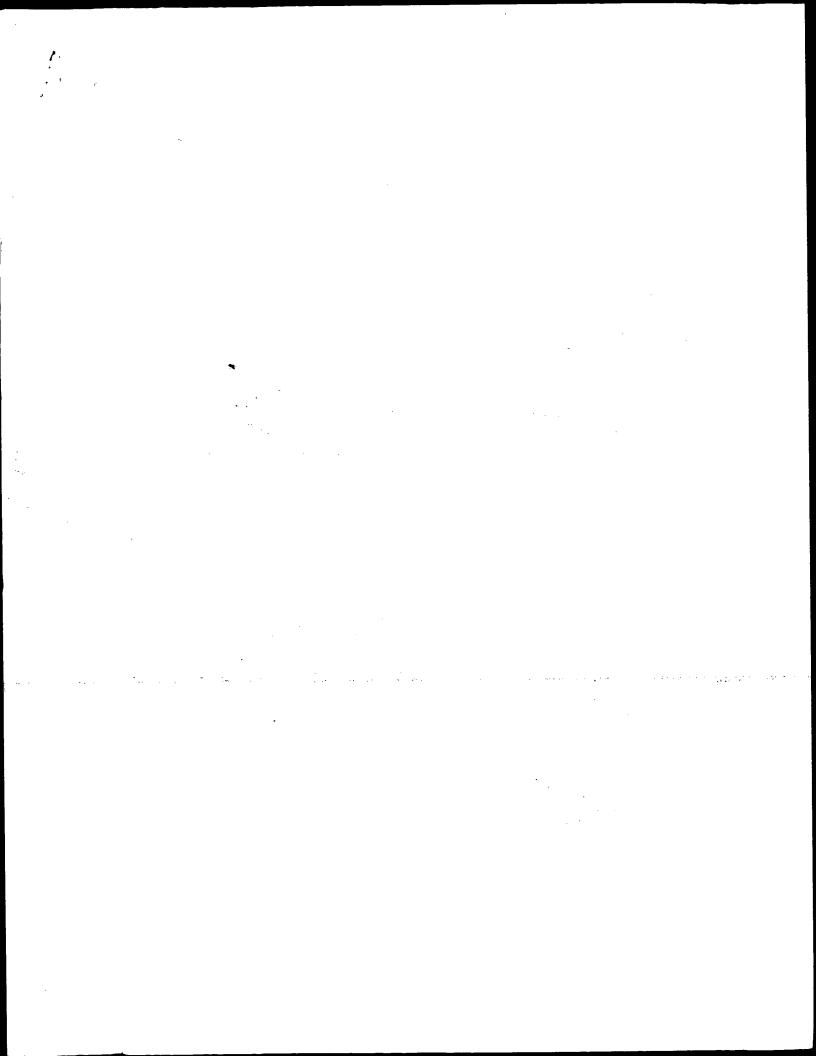
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Best Local :
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                                                                                                                                348
          267
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                                                                                                                                                                                          288 ccccamatctgccgtgtatgtggggacaaggccactggctatcacttcaatgtcatgaca 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        588 ctgggagtgcaggggctgacagaggagcagcggatgatgatcagggagctgatggacgct 647
                                                                                                                                                                                                                                                                      Match 5.0%; Local Similarity 65.1%;
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| CCCTTC---ANTGGAGATTGCCGCATCACCAAGGACAACCGGCGACACTGCCAGGCCTGC 323
                                                                                TOTGAAGGCTGCAAGGGTTTCTTCAGGCGGAGCATGAAGCGCAAGGCCCTGTTCACCTGC 266
                                                                                                            tgtgaaggatgcaagggctttttcaggagggccatgaaacgcaacgcccggctgaggtgc 407
                                                                                                                                                                  CCTCGGATCTGTGGAGTGTGTGGAGACCGAGCCACGGGCTTCCACCTTCAACGCTATGACC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLAM8934 row: a column: 11
High quality sequence start: 2
High quality sequence stop: 685.
Location/Qualifiers
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Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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BE573696.1 GI:9817416
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Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1053)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="TLMAGE:3710866"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH*

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501 CCCACCACAAGACCTACGACCCCACCTATGCCGACTTCCGGGACTTCCGGGCCTCCA 556
                       646 ctcagatgaaaacctttgacactaccttctcccattttcaagaatttccggctgcca 701
                                                                                        324 CGGCTCAAACGCTGCGTGGACATCGGCATGATGAACGGAGTTCATCCTCACAGACTGAGG 383
                                                                   444 GTCTGAG---GCCCAAGCTGTCTGAGGAGCAACAGCACATCATCGCCATCCTGCTCGATG
                                                                                                                                                                                                                                                    468
                                                                                                                                                             ccgtggaggegaggcgttgatcaagcggaagaaaagtgaacggacagggactcagc 585
                                                                                                                                                                                                                              cgcctgcgcaagtgcctggagagcggcatgaagaa-ggagatgatcatgtccgac-gagg 525
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Search completed: February 18, Job time: 17063 sec 2001, 19:19:59



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Result
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pred. No. 1s the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Comp
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US-08-592-383-5

US-08-592-383-5

US-08-592-383-4

US-08-592-383-4

US-08-342-411A-3

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ALIGNMENTS

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RESULT 1
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APPLICANT: Deluca, Hector F.

APPLICANT: Ross, Troy K.

APPLICANT: Prahl, Jean M.

TITLE OF INVENTION: Method of Producing
TITLE OF INVENTION: 1,25-Dlhydroxyvitamin D3 Receptor Protein
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

***CORRESPONDENCE ADDRESS:
TOPOLOGY: linear
MOLECULE TYPE: CONA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
PUBLICATION INFORMATION:
AUTHORS: Burmester, James K.
AUTHORS: Wiese, Russell J.
AUTHORS: Medda, No. 5260199uyo
AUTHORS: DeLuca, hector F.
TITLE: Structure and regulation of the rat
                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
REFERENCE/DOCKET NUMBER: 96-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 414-277-57,15
                                                                                                                                                                                                                                                                                                          TELEFAX: 414-277-5774
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 2043 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,736B
FILING DATE: 19910730
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: double
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411 East Wisconsin Avenue
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JOURNAL:

1,25-dihydroxyvitamin D3 receptor Proc. Natl. Acad. Sci. U.S.A.

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Best Local Similarity
Matches 629; Conserv
1173 ctgcagctgcatgaggaggagtatgtgctgatgcaggccatctccctcttctccccagac 1232
                                                                             1113 ggtggcttccagcaacttctactggagcccatgctgaaattccactacatgctgaagaag 1172
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PAGES: 9499-9502
DATE: December-1988
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                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 414-277-5774
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                          PUBLICATION INFORMATION:
                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                   HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ross, Troy K.
APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method of Producing
TITLE OF INVENTION: 1,25-Bihydroxyvitamin
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1353 atcatggctatgctcaccgagctccgcagcatcaatgctcagcacacccagc 1404
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                                                                                                 AUTHORS:
AUTHORS:
AUTHORS:
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                                         AUTHORS:
                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID STRANDEDNESS: doub TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Schwartz, Carl R. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                               ORGANISM:
                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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CLASSIFICATION: 435
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STATE: Wisconsi
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: Pike, J.W.
: Shine, John
: O'Malley, Bert W.
: Cloning and expression of full-length encoding human vitamin D receptor
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                                                                                           Hughes, Mark
Crisp, Tracey M.
Mangelsdorf, David
Haussler, Mark R.
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414-277-5774
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                                                                                                                                                                    Baker, Andrew R. McDonnell, Donal
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Proc. Natl. Acad. Sci. U.S.A.

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; JOURNAL: Proc. Nat
; VOLUME: 85
; PAGES: 3294-3298
; DATE: May-1988
US-07-737-736B-5
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Best Local Sim
Matches 638;
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Local Similarity 55.1%;
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atgctgaagaagctgcagctgcatgaggaggagtatgtgctgatgcaggccatctccctc
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                                                                         gaagacactgcaggtggcttccagcaacttctactggagcccatgctgaaattccactac 1160
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                                                   GACGTGACCAAAGCCGGACACAGCCTGGAGCTGATTGAGCCCCCTCATCAAGTTCCAGGTG 1069
                                                                                                                        TTCACCATGGACGACATGTCCTGGACCTGTGGCAACCAAGACTACAAGTACCGCGTCAGT 1009
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                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/843,35
FILING DATE: FEBRUARY 26, 199
ATTORNEY/AGENT INFORMATION:
NAME: PAUL T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
TELEPHONE: (617) 542-8906
TELEPHONE: 017 542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50z or 55SX
COMPUTER: IBM PS/2 Model 50z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION UNDBER: US/08/459,489
FILING DATE:
CLASSIFICATION: 435
                                                                                           Matches 327; Conservative
                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: CAR RECEPTORS TITLE OF INVENTION: MOLECULES AND NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                  TYPE: nucleic acid
TYPE: nucleic single
STRANDEDNESS: single
TYPOTOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                       889 ccctgctgccccacatggctgacatgtcaacctacatgttcaaaggcatcatcagctttg 948
739 CTCTGGTCACACTTCGCAGACATCAACACTTTCATGGTACTGCAAGTCATCAAGTTTA 798
                                                                                                               Match 6.18;
Local Similarity 57.58;
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CAR RECEPTORS
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cy 26, 1992
                                                                                         Score 170.6; DB 1;
Pred. No. 5.8e-28;
0; Mismatches 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08458686
Patent No. 5710017
GENERAL INFORMATION:
APPLICANT: DAVID D. MOORE et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
INFORMATION FOR SEQ ID NO:
                                                                                              FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: ISM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
                                      REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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             TELEPHONE: (617) 542-8906
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                                                                                                                                                                                                                                                                                                                         COUNTRY:
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3ER: 00786/126001
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Best Local :
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                                                                                                                                                       NUMBER OF SEQUENCES:
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LENGTH: 1450.
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                                                               COUNTRY:
                                                                                STATE:
                                                                                                            STREET:
                                                                                                                           ADDRESSEE:
                                                                                               Boston
                                                                U.S.A.
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Sequence 1, Application US/07843350C Patent No. 5756448
GENERAL INFORMATION:
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 35.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
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Pred. No. 5.8e-28;
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RESULT 6
PCT-US93-01559-1
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Best Local Similarity 57.5%;
Matches 327; Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/843,350C
FILING DATE: February 26, 1992
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PRIOR APPLICATION DATA:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                 tacacccctttgctacgcccctcatgcag 1454
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Pred. No. 5.8e-28;
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Sequence 1, Application PC/TUS9301559

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PCT-US93-01559-1
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REFERENCE/DOCKET NUMBER: 00786/126001
REFERENCE/DOCKET NUMBER: 00786/126001
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 542-5070
TELEPAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1450
TYPE: NUCLEIC ACID
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Best Local Similarity 57.5%;
Matches 327; Conservative
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APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IEM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IEM P.C. DOS (Version 3.30)
SOFTWARE: Wordberfeet (Version 5.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
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ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/843,350
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1099 CCCAGAGAGATGAGATTGATCAGCTGCAAGAGGAGATGGCACTGACTCTGCAAAGCTACA 1158
                           1246 tgcagcaccgcgtggtggaccagctgcaggagcaattcgccattactctgaagtcctaca 1305
                                                                                                                                                                                                                                      1126 aacttctactggagcccatgctgaaattccactacatgctgaagaagctgcagctgcatg 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCAGCTGTGGAAATCTGTCACATCGTACTCAATACCACTTTCTGTCTCCCAAACACAAA 918
                                                                                                                              aggaggagtatgtgctgatgcaggccatctcccttcttctccccagaccgcccaggtgtgc 1245
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; LOCATION:
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ARCD154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR: TITLE OF INVENTION: COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 38
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APPLICANT: SONG, Ching
                                                                                                                  CORRESPONDENCE ADDRESS:
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405 tgccccttccggaagggcg---cctgcgagatcacccggaagacccggcgacagtgccag
                                                 374 GACTGCGAAGGCTGCAAGGGCTTCTTCCGGCGCAGTGTGGTCCGTGGTGGGGCCCAGGCGC 433
                                                                      345 acatgtgaaggatgcaagggctttttcaggagggccatgaaacgcaacgcccggctgagg 404
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-NOV
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                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1898 base pairs
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P.O. Box 4433
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                                                                                                                                                                                      Score 97.6; DB 1;
Pred. No. 2.9e-12;
0; Mismatches 569;
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                                                                                                                                                                                                                       Length 1898;
                                                                                                                                                                                       Indels 76;
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                                                                               gcatccaggacatacacccctttgctacgcccctcatgcaggagttgttcggcatcacag 1473
                                             CCTTGCGGCTCCAGGACAAGAAGCTGCCGCCTCTGCTGTCGGAGATCTGGGGACGTCGACG 1448
                                                                                                                                       TGAAGCTGGTGAGC-----CTGCGCACCCTGAGCTCTGTGCACTCGGAGCAGGTCTTCG 1388
                                                                                                                                                                    tcatggctatgctcaccgagctccgcagcatcaatgctcagcacacccagcggctgctgc 1413
                                                                                                                                                                                                                                TGCTGTCCTACACGCGCTACAAGAGGCCGCAGGACCAGCTGCGCTTCCCGCGCATGCTCA 1334
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                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                           Matches
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Patent No. 5871916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/JP95/01909
FILING DATE: 21-SEPT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tellyence F. Chapman
REGISTRATION NUMBER: 32549
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APPLICATION NUMBER
FILTER
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MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP6-226270
FILING DATE: 21-SEPT-1994
                   271 atgaggaagtcggaggtccccaaatctgccgtgtatgtggggacaaggccactggctatc 330
                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
438 CCCCGAAGATGCTGGGCCACGAGCTTTGCCGTGTGTGGGGGACAAGGCCTCCGGCTTCC 497
                                                                378 CAGACTGGGTCATCCCAGATCCCGAAGAGGAACCAGAGCGCAAGCGAAAGAAGAAGGCCCAG 437
                                                                                            211 ctgactttgtacactgtgaggacacagagtctgttcctggaaagcccagtgtcaacgcag 270
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                      LIBRARY:
LIBRARY:
                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 206..1591
IDENTIFICATION METHOD: experimental examination
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                       215;
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                                                                                                                                                                                                                                                                                                                    Human mammary gland cDNA
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                                                                                                                                    Score 97.6; DB 2;
Pred. No. 2.9e-12;
0; Mismatches 174;
                                                                                                                                                                  Length 1979;
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US-08-330-518-1
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   Query Match
Best Local Similarity
Matches 215; Conserv
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                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 11FORMATION:
NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,518
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                                                                                                                     ANTI-SENSE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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126 East Lincoln Avenue
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Vogel, Robert
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                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                           single
                     3.5%;
54.8%;
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                                                                                                                                                                                                                                                                                                                                                          36,502
Score 97.6; DB 1; Length 2030; Pred. No. 3e-12; O; Mismatches 174; Indels 3
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US-08-330-283-1
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                                                                                                                      TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schmidt, Azri
APPLICANT: Vogel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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             HYPOTHETICAL:
                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                            TOPOLOGY:
                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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126 East Lincoln Avenue
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Holloway, M. Katharine
Rodan, Gideon
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Schmidt, Azriel
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                                                              linear
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                                        DNA (genomic)
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US-08-646-248-1
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Patent No. !
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                                APPLICATION NUMBER: US/08/646,248
FILING DATE: 14-MAY-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,283
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: DOLAN, Catherine A.
REGISTRATION NUMBER: 36,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Vogel, Robert
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co.,
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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nes 215; Conserv
                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rahway
                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGCAAGTGCCAGCAGTGCCGCCTGCGCAAGTGCAAGGAGGCAGGGATGAGGGAGCAGT 716
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Schmidt, Azriel
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54.8%;
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Pred. No. 36
                        19327
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TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDENESS: single

TOPOLOGY: linear

TELEPHONE:

(908) 594-4283 908) 594-4720 R SEQ ID NO: 1:

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Best Local Similarity 54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9513924 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
                                                                                                                                                                                                                                                                                           APPLICANT: Vogel, Robert
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
                                                                                                                                           CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
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APPLICATION NUMBER: PCT/US95/13924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGTCCTTTCTGAAGAACAGATCCGGAAGAAGAAGATTCGGAAACAGCAGCAGCAGCAGGAGT 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACAGTCACAGTCGCAGTCACCTGTGGGGCCG 808
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                                                                                                                                                                                                                                                                                                                                                                                                     Friedman, Eitan
Holloway, M. Katharine
Rodan, Gideon
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Schmidt, Azriel
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Pred. No. 3e-12;
0; Mismatches 174; Indels 3
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RESULT 13 PCT-US95-13931-1

567 716 656

596

Sequence 1, Application PC/TUS9513931 GENERAL INFORMATION:

APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

ADDRESSEE: Merck & Co., L....
STREET: 126 East Lincoln Avenue

COMPUTER READABLE FORM

COUNTRY: US ZIP: 07065-0907 CITY: Rahway STATE: New Ju

New Jersey

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.5%; Score 97.6; DB 4; Length 2030; Best Local Similarity 54.8%; Pred. No. 3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3809
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Quagliato, Carol S
REGISTRATION NUMBER: 35,
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HYPOTHETICAL: NO
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                      568 aacggacagggactcagccactgggagtgcag 599
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                                                                                  717 GCGTCCTTTCTGAAGAACAGATCCGGAAGAAGAAGATTCGGAAACAGCAGCAGCAGGAGT 776
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                                                                                                                                                                                                  ggcgacagtgccaggcctgcctgcgcaagtgcctggagagcggcatgaaggagag 507
CACAGTCACAGTCGCAGTCACCTGTGGGGCCG 808
                                                                                                                                                                         GGCGCAAGTGCCAGCAGTGCCGGCTGCGCAAGTGCAAGGAGGCAGGGATGAGGGAGCAGT
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MEDIUM TYPE:

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RESULT 14
PCT-US94-12883-3
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; ANTI-SENSE:
PCT-US95-13931-1
                                                                                                                                                                        Sequence 3, Application PC/TUS9412883 GENERAL INFORMATION:
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Best Local Similarity 54.8%;
Matches 215; Conservative
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                                                                    TITLE OF INVENTION: UB
TITLE OF INVENTION: ME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 19316 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                      STREET:
STATE:
                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/13931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTACAACGTGCTCAGCTGCGAAGGCTGCAAGGGCTTCTTCCGGCGCAGTGTGGTCCGTG 596
                  Houston
                                      P.O. Box 4433
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                                                      Arnold, White & Durkee
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                               UBIQUITOUS NUCLEAR RECEPTOR: COMPOSITIONS AND METHODS
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; MOLECULE TYPE: DNA (genomic)
PCT-US94-12883-3
                                                                                                     Sequence 3, Application US/08095728B Patent No. 5843642 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 187; Conservative
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Best Local Similarity 58.8%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
                                      APPLICANT:
APPLICANT:
APPLICANT:
                         APPLICANT:
  TITLE OF INVENTION:
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TELEPHONE: ($12) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         582 cagccactgggagtgcag 599
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                                                                                                                                                                                                                                                 529 CAGTCACCTGTGGGGCCG 546
                                                                                                                                                                                                                                                                                                                                469 GAACAGATCCCGAAGAAGAAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCG
                                                                                                                                                                                                                                                                                                                                                                                                              409 CAGTGCCGGCTGCGCAAGTGCAAGGAGGCAGGGATGAGGGAGCAGTGCGTCCTTTCTGAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                     462 gcctgccgcctgcgcaagtgcctggagagcggcatgaaggaggaggatgatcatgtccgac 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 ggtccccaaatctgccgtgtatgtggggacaaggccactggctatcacttcaatgtcatg 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AGCTGCGAAGGCTGCAAGGGCTTCTTCCGGCGCAGTGTGGTCCGTGGTGGGGGCCAGGCGC 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BARBARA S. KITCHELL REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                  gaggccgtggaggaggcgggccttgatcaagcggaagaaaagtgaacggacagggact 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATGCCTGCCGGGGTGGCGGAACCTGCCAGATGGACGCTTTCATGCGGCGCAAGTGCCAG 408
                   FRANKEL,
                                      DMITROVSKY, ETHAN
WARRELL JR, RAYMOND P
MILLER JR, WILSON H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
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METHODS FOR THE DETECTION AND
                       STANLEY
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Pred. No. 3.5e-12;
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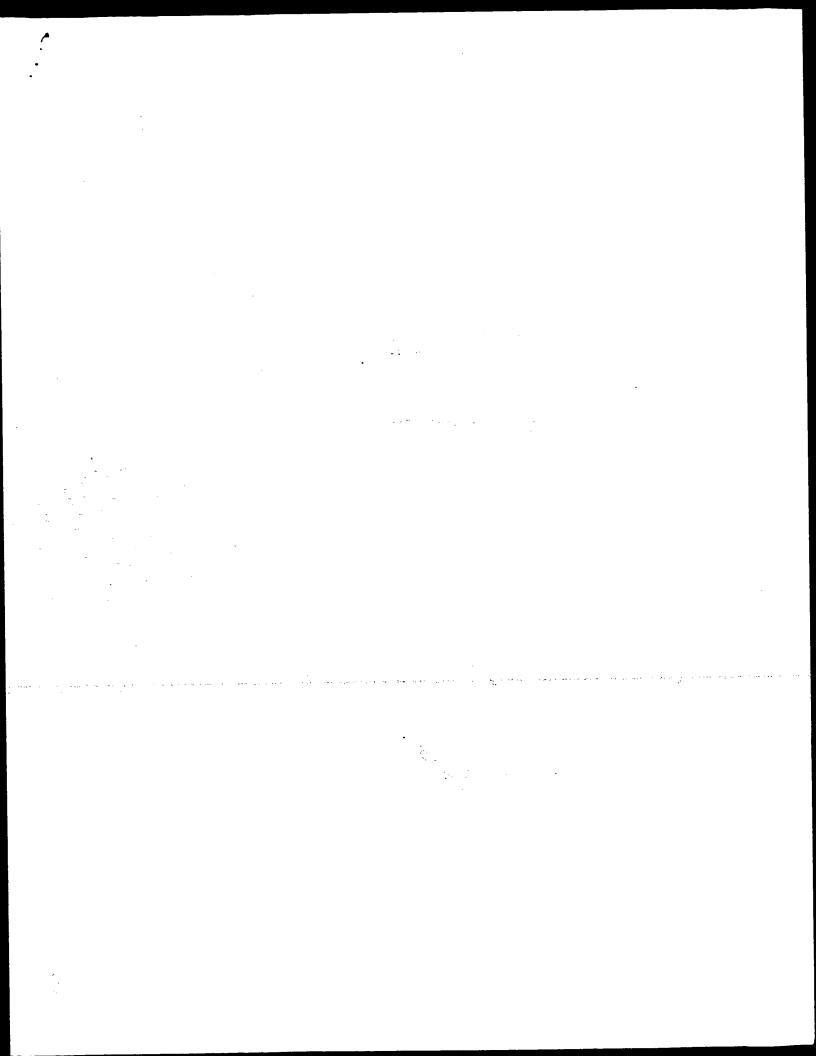
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; NAME/KEY: CDS
; LOCATION: 103..1488
; OTHER INFORMATION:
US-08-095-728B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.3%; Score 91.4; DB 2; Length 2928; Best Local Similarity 50.8%; Pred. No. 7.1e-11; Matches 302; Conservative 0; Mismatches 281; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 278-(
TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1247 gcagcaccgcgtggtggaccagctgcaggagcaattcgccattactctgaagtcctacat 1306
                                            1071 TGCGGAGACGGGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGACCGCCAGGACCTGGA 1130
                                                                           1187 ggaggagtatgtgctgatgcaggccatctctccctcttctccccagaccgcccaggtgtgct 1246
                                                                                                                                                                                                                                                                                     1070
                                                                                                                                   1010 ggccgctttcgagctgtgtcaactgagattcaacacagtgttcaacgcggagactggaac 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38694-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                          951 CATGACCTTCTCGGACGGGCTGACCCTGAACCGGACCCAGATGCACAACGCTGGCTTCGG 1010.
                                                                                                                                                                                                                                                                                                                                                                                                        831 CAAGCAGCTGCCCGGCTTCACCACCCTCACCATCGCCGACCAGATCACCCTCCTCAAGGC 890
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NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 21-JU
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                          1424 catacacccctttgctacgcccctcatgcaggagttgttcggcatcacaggtagc 1478
                                                                                               1245 TACTGACCTGCGAAGCATCAGCGCCAAGGGGGGCTGAGCGGGTGATCACGCTGAAGATGGA 1304
                                                                                                                                                                                                                                                                                                  1131 GCAGCCGGACCGGGTGGACATGCTGCAGGAGCCGCTGGAGGCGCTAAAGGTCTACGT 1190
                                                                                                                                      1367 caccgagctccgcagcatcaatgctcagcacacccagcggctgct---gcgcatccagga 1423
                                                                                                                                                                                                1191 GCGGAAGCGGAGGCCCAGCCCCCACA-----TGTTCCCCAAGATGCTAATGAAGAT 1244
                                                                                                                                                                                                                                1307 tgaatgcaatcggccccagcctgctcataggttcttgttcctgaagatcatggctatgct 1366
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Search completed: February 18, 2001, 16:49:45 Job time: 8404 sec



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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    Pred. No. 1s the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2586.2
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1866.6
1466.6
1422
1330.2
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2: /cgn2_2/gcgd
3: /cgn2_2/gcgd
4: /cgn2_2/gcgd
5: /cgn2_2/gcgd
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92.3
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2802
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| Cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
| Cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
| Cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
| Cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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  DB
    222222222222
                     X56242
X59975
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Z07997
X89080
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Human nNR7 CDNA. r
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DNA encoding an in
SEQ ID 12 of JP111
                                                                                                                                      Human vitamin D re
Human nNR7-1 cDNA.
DNA encoding an in
Human vitamin D re
DNA encoding an in
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Human myl/RAR-alph	V64990		3036		91.4	S
Human PML/RARalpha	V20474		3036		91.4	4
myl/RAR-alpha fusi	Q29334		3036		91.4	w
DNA of clone phrar	N90124		2940	3	91.4	N
Human RAR-alpha cD	V64991		2928		91.4	ш
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NER receptor poten	T30031		2030	٠	•	œ
Human steroid rece	T18996		2030	٠		7
Human recombinant	Q63134		2030	٠	•	σ
Human foetal lung	T27616		1979	٠	•	ഗ
DNA encoding human	T79634		1898		•	•
Mouse nuclear rece	X80217		468		•	ω
Mouse CAR receptor	X24003		1361	•	•	N
Human CAR receptor	X23994		1450		•	,_
Human CAR receptor	Q46131	14	1450	6.1	170.6	0
Constitutively act	T92305		1450		•	φ
Mouse nuclear rece	X80215		1280		•	œ
cDNA encoding rat	V03130		1404		•	7
Human vitamin D re	X16597		1404	•	•	σ
ğ	X34790.		. 1534	•	-	G
	X16606		3382	٠	ω	_
cDNA encoding rat	V18518		3382	8.4	ω	ω
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=	207545		3510	9.7	272.8	8
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Nucleotide sequenc	X34789		1382	9	•	G
vitamin D	Q51425		2043	10.0	•	42
cDNA encoding rat	V03129		1960	10.0	•	ω

ALIGNMENTS

16-JUL-1999 (first:entry)

X56243 standard; cDNA; 2802 BP.

Human; vitamin D receptor related protein; VDRR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia; hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour; Human vitamin D receptor related gamma 2 protein encoding cDNA New vitamin D receptor related (VDRR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis WPI; 1999-302508/25. P-PSDB; Y09516; Berkenstam A, (PHAA) PHARMACIA & UPJOHN AB 31-MAR-1998; 14-OCT-1997; 31-AUG-1998; 22-APR-1999. Homo sapiens. hyperproliferative skin disorder; hyperthyroidism; ss WO9919354-A1 Dahlberg M; 98SE-0001148. 97SE-0003745. 98WO-SE01548

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Claim 2; Page 21-22; 35pp; English.
```

The present sequence encodes a human vitamin D receptor related (VDRR) CC polypeptide. Human VDRR polypeptides and substances which affect VDRR CC signal transduction, can be used for treating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a CC medicament for treating the following conditions: obesity, diabetes, CC ancrexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or CC hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and CC malign tumours, hyperproliferative skin disorders or hyperthyroidism. CC Nucleic acid vectors encoding for expression of a VDRR polypeptide can CC be used for treating metabolic, proliferative or inflammatory conditions, CC by introducing them into a mammal. The introduced nucleic acid is then CC capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or CC antagonist can be used for the manufacture of a medicament for treating CC metabolic, proliferative or inflammatory condition.

CC N.B. The specification specifically claims the VDRR nucleic acid and CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures are given in the specification.

Sequence 2802 BP; 723 A; 715 C; 755 G; 609 T; 0 other;

Query Match 100.0%; Score 2802; Best Local Similarity 100.0%; Pred. No. 0; Matches 2802; Conservative 0; Mismatches

DB

20; Length 2802; Indels

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tcagagaggc&aggttgccctttccttttaaaaggccctgtggtctggggagaaatccct 1800	1741	Qy
gtagggagtgaagccacagactcttacgtggagagtgcactgacctgtaggtcaggacca 1740	1681	ర్జ
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cccagcctgctcataggttcttgttcctgaagatcatggctatgctcaccgagctccgc	1321	Qy
1 tggaccagctgcaggagcaattcgccattactctgaagtcctacattgaatgcaatcggc 1320	1261	밁
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	1143	Db
catyctyaanttccactacatyctyaayaayctycayctycatyayyayyaytatyty		Ϋ́O
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gccggctgtcctactgcttggaagacactgcaggtggcttccagcaacttctactggag		Qy
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This invention describes the isolation of the novel human nuclear receptors nNR7 or nNR7-1. The nNR7 and nNR7-1 proteins are useful in the identification of downstream target genes and ilgands regulating its activity. The nuclear receptor is involved in the regulation of in vivo cell proliferation and/or cell development. The nNR7 and nNR7-1 polynucleotides, expression vectors and host cells are useful for the recombinant production of the protein.
                                                                                                                                             WPI;
                                                                                                                                                                                                                          11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                 nNR7; nNR7-1; no identification;
                                                                                                                                                                                                                                                                                                                                                                                              Human
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12-DEC-1997;
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                                                                                                                 DNA encoding human nuclear receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding an intranuclear receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment;
                                                                                                                                                                             The present sequence encodes a human intranuclear receptor protein. The nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment
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The present polypeptide.

sequence Human

VDRR

encodes a human DRR polypeptides

vitamin D receptor related (VDRR) and substances which affect VDRR

CC signal transduction, can be used for treating metabolic, proliferative cor inflammatory conditions. They can be used in the manufacture of a CC medicament for treating the following conditions: obesity, diabetes, CC anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or CC hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and CC malign tumours, hyperproliferative skin disorders or hyperthyroldism.

CC Nucleic acid vectors encoding for expression of a VDRR polypeptide can CC be used for treating metabolic, proliferative or inflammatory conditions, by introducing them into a mammal. The introduced nucleic acid is then CC capable of transforming a cell in vivo and then polypeptide is expressed.

CC A substance affecting VDRR signal transduction, such as an agonist or CC antagonist can be used for the manufacture of a medicament for treating CC metabolic, proliferative or inflammatory condition.

CC N.B. The specification specifically claims the VDRR nucleic acid and CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures are given in the specification.

Sequence 2910 BP; 765 A; 728 C; 780 G; 636 T; 1 other;

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WPI; 1999-419349/35. P-PSDB; Y21799.

Blumberg B, Evans RM;

New steroid and xenobiotic receptor, used to identify modulators for controlling metabolism of steroids and xenobiotics, e.g. reducing their toxicity

Claim 10; Fig 1A; 83pp; English.

CC The invention relates to a novel nuclear receptor polypeptide, designated CC SXR (steroid and xenobiotic receptor). SXR (i) forms a heterodimer with CC retinoid X receptor (RXR), (ii) binds to a direct or inverted repeat CC response element motif based on the half-site ACTTCA, (iii) activates CC transcription through response elements present in steroid-inducible P450 CC genes, in response to a wide variety of natural and synthetic steroid CC hormones and (iv) is prominently expressed in liver and intestine. SXR CC regulates expression of catabolic enzymes, in response to many different CC steroids, and thus affects metabolism. SXR is a broad specificity, low-cc affinity receptor for reducing excessive levels of steroids in the CC circulation. (Ant)agonists of SXR are used to regulate metabolism of CC steroids particularly phytoestrogens or calcium-channel blockers, to CC reduce steroid toxicity in subjects being treated with steroids, e.g. in CC cases of tuberculosis (treated with rifampin and related compounds), CC treated with vitamin K), or to slow metabolism of therapeutic steroids. CC Also, modulating endogenous SXR is used to treat disease, particularly an agonist is used where endogenous steroid levels are excessive (e.g. CC cushing syndrome, virilism and hirsutism in women; polycystic ovarian CC dehydrogenase deficiency, or breast, colorectal or prostatic cancer), while antagonists are used where endogenous steroid levels are too low. CC cells that express SXR are used to identify compounds likely to be involved in undesirable drug interactions. Antibodies specific for SXR cc antagonist. The present sequence represents the longest SXR CDNA clone cc encoding the SXR polypeptide.

Sequence 2068 BP; 520 A; 541 C; 586 G; 420 T; 1 other;

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Pred. No. 1.1e-260;
0; Mismatches 0;
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Best Local Similarity
Matches 430; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a human intranuclear receptor protein. The nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New intranuclear receptor protein - useful for drug development and diagnosis and treatment of disease
 11-JUN-1998
                          V03129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 644 BP; 175 A; 161 C; 193 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 32; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-350330/30
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                                                    V03129 standard; cDNA; 1960 BP
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                                                                                                                                                                                                                                    ggaagacccggcgacagtgccaggcctgccgcctgcgcaagtgcctgggagagcggcatga 498
                                                                                                                                                                                                                                                                                          | ccatgaaacgcaacgcccggctgaggtgccccttccggaagggcgcctgcgagatcaccc
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                                                                                                                                                                    agaaggagatgatcatgtccgacgaggccgtggaggagaggcgggccttgatcaagcgga
                                                                                                                                                                                                                        ggaagacccggcgacagtgccaggcctgccgcctgcgcaagtgcctggagagcggcatga
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(first entry)
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Pred. No. 4.5e-79;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a vitamin D receptor isoform protein - useful for density determination and for screening substances for vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-051917/05.
P-PSDB; W47509.
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                                                                                                                                                                                                                                                                                                                                            Sequence 1960 EP; 432 A; 620 C; 497 G;
                                                                                                                                                                                                                                                                                                                                                                                   The isoform protein can be used to diagnose bone density disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 46pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                     screen for substances having potential vitamin D-like activity
                                                                                                                                                                                  tgtgaaggatgcaagggctttttcaggagggccatgaaaacgcaacgcccggctgaggtgc 407
                            gtggaggagaggcgggccttgatcaagcggaagaaaagtgaacggacagggactcagcca
                                                                              cccttccggaagggcgcctgcgagatcacccggaaggacccggcgacagtgccaggcctgc
            gtacagcgtaagggagatgataatgaagagaaaagggaagaggccttgaaggacagt
                                                                                                                   cccttc---aatggagattgccgcatcaccaaggacaaccggcgacactgccaggcctgc
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                                                                                                                                                                                                                       ccccggatctgtggagtgtgtggagaccgagccacaggcttccacttcaatgctatgacc 131
                                                                                                                                                                                                                                                                            629;
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10.08;

0 Score Pred.

Mismatches ŏ.

Indels Length

Gaps

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527

308

467 191

248

278.8; DB 19;

1960; 21;

1.1e-48 482;

411 T; 0 other;

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Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                      Rat; vitamin D receptor; isoform protein; VDR1; dominant negative receptor; signal transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding rat vitamin D receptor (VDRO).
                                                                                                                                                                                                                                                                                                                                                                                     density disorder; screening; ds.
                                                      CHUGAI
                  Ueno K;
                                                                         PHARM CO LTD.
                                                      SEIYAKU KK
                                                                                                             96JP-0194179
                                                                                                                                               97WO-IB00947
                                                                                                                                                                                                                                                                         Location/Qualifiers
12..1283
/*tag= a
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   Key
                                               1,25-dihydroxyvitamin insect host; ds.
                                                                                 Rat vitamin
                                                                                                       16-MAY-1994 . (first entry)
                                                                                                                                051425
                                                                                                                                                     Q51425 standard; cDNA; 2043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2043 BP; 448 A; 647 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant prodn. of 1,25-di:hydroxy-vitamin=D3 - using expression system comprising insect cell recombinant virus contg. foreign DNA
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569 atggacggaagtacagggagctattctccaaggcccacactcagcttctccggggaactcc
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Claim 4; Fig 6; 56pp; English New polynucleotides which encode novel isoforms of the human vitamin D receptor or yariant transcripts for hVDR

The invention relates to isolated polynucleotides which encode novel isoforms of the human vitamin D receptor (VDR) or variant transcripts for hVDR. The polynucleotides are useful in methods for detecting agonist and for antagonist compound of a VDR isoform. An increase or decrease in activity of the receptor may be detected by measuring changes in interactions with known cofactors (e.g. SRC-1, GRIP-1 and TFIIB) or unknown cofactors (e.g. through use of the dual hybrid system). The polynucleotides shown in x34787, x34791 and x34792 (corresponding to hVDR exon sequences) may be useful as probes for the detection of VDR variant transcripts and for assessing cell or tissue-specific expression of variant transcripts. The present sequence represents the nucleotide sequence of hVDR gene transcript 9.

Sequence 1382 EP; 310 A; 409 C; 379 G; 284 T; 0 other

Query Match
Best Local Similarity

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g Ş 밁 Ş 밁 Ş 닭 Ş 밁 Ş 밁 Š 밁 S 밁 S 밁 Ş 밁 Ş 밁 δÃ Matches 930 633 513 456 588 396 336 468 279 408 219 348 159 813 753 870 693 810 750 573 708 648 528 tgtgaaggatgcaagggctttttcaggagggccatgaaacgcaacgcccggctgaggtgc ccccaaatctgccgtgtatgtggggacaaggccactggctatcacttcaatgtcatgaca caaaaggtcattggctttgctaagatgataccaggattcagagacctcacctctgaggac aaaggcatcatcagctttgccaaagtcatctcctacttcagggacttgcccatcgaggac ctagagctgtcccagctctccatgctgccccacctggctgacctggtcagttacagcatc gtgaatgatggtggagggagccatccttccaggcccaactccagacacactcccagcttc cttagcagtggctgcgagttgccagagtctctgcaggcccc-----a ctgggagtgcaggggctgacagaggagcagcggatgatgatcagggagctgatggacgct gtggaggagaggcggggccttgatcaagcggaagaaaagtgaacgggacagggactcagcca cggctcaaacgctgtgtggacatcggcatgatgaaggagttcattctgacagatgaggaa cgcctgcgcaagtgcctggagagcggcatgaaggagatgatcatgtccgacgaggcc cccttccggaaggcgcctgcgagatcacccggaagacccggcgacagtgccaggcctgc tgtgaaggctgcaaaggcttcttcaggcgaagcatgaagcggaaggcactattcacctgc ccccggatctgtggggtgtgtgtggagaccgagccactggctttcacttcaatgctatgacc 218 ggcgggaaagagatcttctccctgctgccccacatggctgacatgtcaacctacatgttc tetetgeagetgegggggggaggatggeagtgtetggaaetaeaaaececeageegaeagt totggggactcctcctcctcctgctcagatcactgtatcacctcttcagacatgatggac tcgagggaagaagctgccaagtggagccaggtccggaaagatctgtgctctttgaaggtc caccataagacctacgaccccacctactccgacttctgccagttccggcctccagttcgt ctgcg--gtgcagaggaagcgggagatgatcctgaagcggaaggaggaggaggccttgaaggacagt cccttc---aacggggactgccgcatcaccaaggacaaccgacgccactgccaggcctgc 638; cagatgaaaacctttgacactaccttctcccatttcaagaatttccggctgccaggggtg tcgtccagcttctccagetctggatctgagtgaagaagattcagatgacccttctgtgacc Conservative -gcccaagctgtctgaggagcagcagcgcatcattgccatactgctggacgcc 0 Score 272.8; DB: Pred. No. 1.7e-47; 0; Mismatches 48; 487; Indels 33 ': Gaps 347 407 467 872 586 812 929 752 692 809 632 749 572 707 647 455 587 395 527 335 278 ٠.

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Search completed: February 18, 2001, 16:55:50 Job time: 8630 sec

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SUMMARIES

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Homo sapiens orphan nuclear receptor (PARI) mRNA,
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Berkenstam,A. Identification of a human nuclear receptor defines a new signaling pathway for CYP3A induction Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12208-12213 (1998) 98445350
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Bertilsson,G., Asman,M., Blomquist,P. and Berkenstam,A.
Direct Submission
Submitted (19-AUG-1998) Cell and Molecular Biology, Medical Nobel
Institute, Karolinska Institute, Doktorsringen2, Stockholm 17177,
Sweden
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//Product="orphan nuclear receptor"
//product="orphan nuclear receptor"
//product="nac64558.1"
//protein_id="nac64558.1"
//db_xref="gI:3769539"
//db_xref="gI:3769539"
//translation="MEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVC
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LESGHKKEMIKASDEAVEERRALIKKKKERTGTGPLGVQGLTEEPQLSHADAQMK
TFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGE
DGSVWNYKKPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVLSYFRDLPIEDQISLL
KGAAFELCQLRENTVENAETGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQ
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1 (bases 1 to 4448)

1 (bases 1, Holloway, J., Hansen, C., Tommerup, N., Aagaard, L. a
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1771. .3144
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Direct Submission
Submitted (31-JUL-1998) Heard D.J., Novo
Genetics, Novo Alle, DK-2880, Bagsvaerd,
                                                                                        Vissing, H.

Identification of a novel protein isoform of the human nuclear recentor PXR/SXR and localization to chromosome 3q12.1
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4337)

1 (bases 1, Holloway, J., Hansen, C., Tommerup, N., Aagaard, L. and
                                                                                                                                                                                                                       nuclear hormone receptor;
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                                           Heard, D.J
                                                                                   hormone receptor PXR/SXR and 13.3
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                                                                                         ACTTACCACCAAACAGTCCAAGAGGCCCAGAAGCAAACCTGGAGGTGAGACCCCAAAGAAA 1861
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GFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAI
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initiates at GUG-1771 5 fold less efficiently
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/tissue_type="intestine"
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3909	3850 TGTGGATGCTGAGCTGTGATGGCGGGCACTGGGTACCCCAAGTGAAGGTTCCCGAGGACAT	뭥
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3849	CMATTTGGATCAAAAGGAG-AAATGATAAGTGACAAAAGCAGCACAAGGAATTTCCCTG	ф
2296	37 acaatttggatcaaaaggagaaaatgataagtgacaaagcagcacaaggaatttccctg	Qy
3790	TCAGATATAGATCCTGAGCTCACAGAGTTTATAGTTAAAAAAAA	당
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3730	TTTGAACACŅTTATTAAGCACCGATAATAGGTAGCCTGCTGTGGGGTATACAGCATTGA	몽
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3670	CAGNAGCTTGGCATGACCTCATTCCGGCCACATCATTCTGTGTCTCTGCATCC	В
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1997	tcccactcgttcccctcctcttccgagctgctttgtgggctcaaggcctgtactcatcg	VΩ
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1937	ccacgtttgttcgcttcctgagtcttttcattgctacctctaatagtcctgtctcccac	Qy
3430	CGACCAAGGATAGGCCATCTGGGGTCTATGCCCACATA	Дb
1877	caaggtgtggaagggaccaagcgaccaaggataggccatctggggtctatgcccacata	Qy
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2950	2891 TCTTGTTCCTGAAGATCATGGCTATGCTCACCGAGCTCCGCAGCATCAATGCTCAGCACA	ф
1398	cttgttcctyaagatcatggctatgctcaccgagctccgcagcatcaatgctcagcaca	Qy

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The human orphan nuclear receptor PXR is activated by compounds that regulate CYP3A4 gene expression and cause drug interactions J. Clin. Invest. 102 (5), 1016-1023 (1998)
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1 (bases 1 to 2146)

1 (bases, D.D., Watson, M.A., Willson, T.M., Moore, J.T. and
                                                                                                                                                                                                                                                                                                                                              Submitted (21-APR-1998) Molecular Endocrinology, Glaxo Wellcome, 5 Moore Drive, RTP, NC 27709, USA
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            /LIANSLATION-"MEVERKESWNHADEVHCEDTESVPGKPSVNADEEVGGPQICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKENIMSDEAVEERRALIKRKKSERTGTQFLGVQGLTEEQRAMIRELMDAQMKTFDTTFSHFKNRRLGPULSGGCELPESLQAPSKREPAAKWSQYRKDLCSLKYSLQLAGEDGSVWNYKPPADSGGREIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEETYLMQAISLFSDDRFGVLQHRVYDQLQEDFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFGITGS"

1 MAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFGITGS

2 605 g 439 t
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acagtgttcaacgcggagactggaacctgggagtgtggccggctgtcctactgct 1098 	1039 tcaacac	Db Qy
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<pre>aaggtctctctgcagctgcggggggaggatggcagtgtctgggabctacbaacccc 858 </pre>	799 ctttgaa: 926 CTTTGAA	₽ Q.
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SEQUENCE, 34 unordered pieces.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                  AC069444.7 GI:9719625
HTG; HTGS_PHASE1; HTGS_DRAFT
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

*NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 34 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
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Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Suggang, R.,
Tabor, P., Taylor, T., Vasguez, L., Vinson, R., Vo, O., Wahbah, M.,
Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A.,
Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
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1 (bases 1 to 16(185)

Muzny,D,M., Adams,C., Balley,M., Barbaria,J., Blankenburg,K.,

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Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,

Forcum-Tansey,J., Frantz,P., Ganer, R., Gorrell,J.H., Gorrell,L.L.,

Chacker, R., Gorrell, J.H., Gorrell, J.H., Gorrell, J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project Information
Center project name: HMTQ
Center clone name: RMTQ
Center clone name: RPIT-169N13
Center clone name: RPIT-169N13
Center clone name: RPIT-169N13
Center stry: Dye-primer Bodiby: 6% of reads
Chemistry: Dye-reminator Big Dye: 94% of reads
Chemistry: Dye-reminator Big Dye: 94% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 13214 bases at least Q40
Consensus quality: 142928 bases at least Q30
Consensus quality: 147607 bases at least Q20
Estimated insert size: 148422; sum-of-contigs estimation
Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Center code: Edit Collège of Medicine
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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49948:
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19805: gap of unknown length
30129: contig of 10324 bp in length
30229: gap of unknown length
40401: contig of 10172 bp in length
l: gap of unknown length is conting of 9347 bp in le gap of unknown length is conting of 9055 bp in le gap of unknown length conting of 5479 bp in le gap of unknown length conting of 6105 bp in le
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source
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                                                     1380 agcatcaatgctcagcaccccagcggctgctgcgcatccaggacatacacccctttgct 1439
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a 32066 c 31244 g 47693
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2519	460 gggctggaatgctgggtatgctctgtgacaaggctacgctgacaatcagttaaacacacc	У 2	Š
2459 67578	400 gtgtgtgatttggtgtaggtaggtotgtttgccacttgatggggcctgggtttgttcctg	у 2 b 67	ko Ko
2399 67638	340 aaggttcccgaggacatgagtctgtaggagcaagggcacaaactgcagctgtgagtgcgt 	67	5 G
2339 67698	280 cacaaggaatttccctgtgtggatgctgagctgtgatggcaggca	. 67	₽. S
2279 67758	220 aacaaacagaaacacaaacaatttggatcaaaaggagaaaatgataagtgacaaaagcag	67	å å
2219 67817	160 tggggtatacagcattgactcagatatagatcctgagctcacagagtttatagttaaaaa	67	å å
2159 67877	100 ttctgtgtctctgcatccatttgaacacattattaagcactgataataggtagcctgctg	67	유 · 5
2099 67937	040 aagccaggaggcctgcaccaaatgtcagaagctttggcatgacctcattccggccacatca 	67	B &
2039 67997	980 caaggcctgtactcatcggcaggtgcatgagtatctgtgggagtcctctagagagatgag 	68	g Q
1979 68057	920 aatagteetgteteeeaetteeeaetegtteeeeteetteegagetgetttgtggget 	68 1	A 참
1919 68117	860 ggggtctatgcccacatacccacgtttgttcgcttcctgagtcttttcattgctacctct	68 1	B 8
1859 68177	800 tcagatcccactaaagtgtcaaggtgtggaagggaccaagcgaccaagggataggccatct 	68	B 5
1799 68237	40 atcagagaggcaaggttgccctttccttttaaaaggccctgtggtctggggagaaatccc 	68	g S
1739 68297	680 tgtagggagtgaagccacagactcttacgtggagagtgcactgacctgtaggtcaggacc 	68	g d
1679 68357	20 atgacagctggctagcattcctcaggaaggacatgggtgccccccacccccagttcagtc	0 684	g S
1619 68417	60 atggacactgccaagagccgacaatgccctgctggcctgtctccctaggggaattcctgct 	, 15	g Q
1559 68477	00 cacetcegagàggcagceagacecagagecetetgagcegceacteegggceaagacag 	, 15	참 경
1499 68537	40 acgcccctcatgcaggagttgttcggcatcacaggtagctgagcggctgcccttgggtga 	685	å å
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Savas, U., Wester, M.R.,
                                                                                                                                                                                                                                                                                                                                                                              Savas, U., Wester, M.R., Griffin, K.J. and Johnson, E.F. Rabbit pregnane X receptor is activated by rifampici Drug Metab. Dispos. 28 (5), 529-537 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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AF182217.1
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Oryctolagus
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/note="PXR"
257. .1492
                                                                                                                                                          /note="PXR; nuclear receptor subfamily 1 group
zinc-finger protein; transcription factor"
                                                                                                                                                                                  /gene="NR112"
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/strain="breed New Zealand white:
/db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                        'tissue_type="kidney"
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Torrey Pines Rd.,
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Best Local Similarity Matches 1200; Conserv
TGGAAGACCCTGAAGGAGGCTTCCAGCAACTTCTTGTGGATCCCTTGCTGAAATTCCACT
                             tggaagacactgcaggtggcttccagcaacttctactggagcccatgctgaaattccact 1158
                                                                                                                            tcaacacagtyttcaacgoggagactggaacctgggagtgtggccggctgtcctactgct 1098
                                                                                                                                                                                                   CCATCGAGGACCAGATCTCCTTGCTCAAGGGAGCCACCCTCGAGCTGTGCCTCCTGAGAT
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                                                                                                                                                                                                                                                                                                     CTACATGTTCAAAGGCATCATCAACTTTGCTAAAGTCATCTCCTACTTCAGGGACTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctttgaaggtétctctgcagctgcggggggaggatggcagtgtctggaactacaaacccc
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 1601)
Jones,S.A., Moore,L.B., Shenk,J.L., Wisely,G.B., Hamilton,G.A.,
McKee,D.D., Tomkinson,N.C., LeCluyse,E.L., Lambert,M.H.,
Willson,T.M., Kliewer,S.A. and Moore,J.T.
The pregnane X receptor: a promiscuous xenoblotic receptor that h
diverged during evolution
Mol. Endocrinol. 14 (1), 27-39 (2000)
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/product="pregnane x receptor"
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/db_xref="taxon:9986"
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gaaattccactacatgctgaagaagctgcagctgcatgaggaggagtatgtgctgatgca
                                                                                                                 tcaactgagattcaacacagtgttcaacgcggagactgggaacctgggagtgtgggccgct
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                                                                                                 CCTCCTGAGATTCAACACCGTGTTCAACGCAGAGACTGGCACTTGGGAGTGTGGTCGGCT
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Mus musculus
AF031814
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                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (29-OCT-1997) Department of Molecular Endocrinology,
Glaxo Wellcome, 5 Moore Drive, RTP, NC 27709, USA
                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1709)
Kliewer, S.A., Moore, J.T., Wade, L., Staudinger, J.L., Jones, S.A., McKee, D.D., Oliver, B.B., Willson, T.M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                       function="steroid signaling"
                                                                                                                                                                                                           /tissue_type="liver"
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e 974.2; DB 1.4. No. 1.2e-193; The matches 273;
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BASE COUNT ORIGIN

Query Match
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Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Direct Submission
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AF151377
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1. 1755
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/strain="Sprague-Dawley"
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                                                                                                    Email: myers@shgc.stanford.edu
Primer A: CCCATCAAGTGGCAAACAGA
Primer B: AGTGAAGGTTCCCGAGGACA
                                                                              STS size: 107
PCR Profile:
                                                                                                                                                         Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
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Mammalia; Eutheria;
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STS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
archosauria: Aves; Neognathae; Galliformes; Phasianidae;
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                                gaatttccggctgccaggggtgcttagcagtggctgcgagttgccagagtctctgcaggc 745
                                                                                                   gatcagggagctgatggacgctcagatgaaaacctttgacactaccttctccccatttcaa
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al Similarity 57.08;
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  GCACTACCAGCCTGCCGTGCGCCTCTGCATCCCCGGCCCGTGCTCCCAGAGCCCACCCGG
                                                                                CATCAGCATCCTCATCGCCGCGCACAAACGCACCTTCGACTCCAGCTTCTCCAGTTCCA
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Handschin, C. and Meyer, U.A.
Direct Submission
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Handschin, C., Podvinec, M. and Meyer, U.A.
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/product="xenoblotic receptor"
/product="xenoblotic receptor"
/product="AAG18374'.1"
/db_xref="Gi:10505179"
/db_xref="Gi:10505179"
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SEEALGRRRALRLORRLAQAQPGGLTAFQGELISILIAHKRTFDSSFSGFGYDYDPN
RLCIPGPCSQSPPGPGVPSASLSPQLDCLDEDVLPUFSILPHFADLSTFMIQQVIKF
RKEIPAPRGLPIDDQISLKKARTIGICQIQFWTVFNEETNAWEQGHCFTIKNGALAG
FQQIYLEPLLKFHISLKKLRLHEAEYVLLVAMLLFSPDHASVTQRDFIDQLQEKVALT
LKSYIDHRHPMPGGRFIYAKLLLILTELQTLKWENTRQILHIQDLSSMTPLLSEIIS"
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/db_xref="taxon:9031"
/tissue_type="liver; kidney; intestine"
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                                                                                  Submitted (29-JUN-1994) to the DDBJ/EMBL/GenBank databases. Yasutomi. Kamei, Kyoto University, Food Science and Technology; Kitashirakawaoiwake-cho, Sakyo-ku, Kyoto, Kyoto 606-01, Japan (Tel:075;753-6263, Fax:075-753-6264)
                                                                                                                                                                                                                                         vitamin D receptor; VDR.
Mus musculus cell_line:3T3-L1 cDNA to mRNA, clone_lib:lambda
Mus musculus
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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DMSWDCGSQDYKYDITDVSRAGHTLELIEPLIKFQVGLKKLMLHEEEHVLLMAICIV
SPDRPGVQDAKLYEAIQDRLSNTLQTYIRCRHPPPGSHQLYAKMIQKLADLRSLNEEH
SKQYRSLSFQPENSMKLTPLVLEVFGNEIS"
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KGFFRSMKRKALFTCPFNGDCRITKDNRRHCQACRLKRCYDIOMMKEFILTDSEYQR
KREMLMKRKEEEEALKDSLRPKLSEGOQHIIAILIDAHHKTYDPTYADFRDFIRAD
VSTGSYSPRPTLSFSGDSSSNSDLYTPSLDMMEPASFSTMDLNEEGSDDPSVTLDLSP
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/protein_id="BAA06737.1"
/db_xref="GI:699619"
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/cell_line="3T3-L1"
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Rat 1,25-dihydroxyvitamin D-3 receptor mRNA,
J04147 J03630
J04147.1 GI:203956
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2 (bases 1 to 2043) &

Burmester, J.K., Wiese, R.J.,
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Burmester, J.K., Maeda, N. and DeLuca, H.F.
Isolation and expression of rat 1,25-dihydroxyvitamin
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                                                                                                                                                                                                                                                                                                                                                                                         DNA
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Rat (Sprague-Dawley) kidney and intestine,
                                                                                                                                                                                                                                                                                 receptor
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                               .Burmester,
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KREMIMKRKEEEALKDSLRPKLSEEQQHIIAILLDAHHKTYDPTYADFRDFRPPVRMD
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                                                                                                                                    /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                           Location/Qualifiers
                                                                                                    1,25-dihydroxyvitamin
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PLSMLPHLADLYSYSIOKVIGFAKMIPGFRDLTSDDQIYTLKASAIEVIMLRSNQSFT
MDDMSWDCGSQDYKYDVDVSKAFTLELIEPLIKFQVGLKKLNLHEEEHVLLMAICI
VSPDRPGVQDAKLVEAIQDRLSNTLQTYIRCRHPPPGSHQLYAKMIQKLADLRSLNEE
HSKQYRSLSFQDENSMKITPLVLEVFGNEIS*

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288 ccccaaatctgccgtgtatgtggggacaaggccactggctatcacttcaatgtcatgaca

Query Match Best Local S Matches 670

Similarity 54.9%;

Score 275; DB 4; Pred. No. 2.7e-47;

Length 2494; Indels

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Gallus gallus
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Cloning and origin of the two forms of chicken vitamin Arch. Biochem. Biophys. 339 (1), 99-106 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus; Luses 1 to 2494)
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CRHPPPGSRLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPEHSMQLTPLVLEVFGNEI
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- Search Completed: February 18 2001 16:48

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                                                                                         SPTREMBL.15:*

1: sp_arches:*

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4: sp_human:*

5: sp_invertebrate

6: sp_manmal:*

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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_plant:*
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sp_vertebrate:*
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sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	score	Query Match	Length	B	븅	Description
<u>.</u>	2494	100.0	473	4	Q9UWW4	Q9unw4 homo sapien
N	2330	93.4	457	۵	Q9UJ26	Q9uj26 homo sapier
ω	2278	91.3	434	4	Q9UJ27	powo
4	2110.5	84.6	420	4	Q9UJ23	123 homo
v	2058.5	82.5	397	4	Q9UJ24	Q9uj24 homo sapien
σ	1973	79.1	379	4	Q90J25	Q9uj25 homo sapien
7	1814.5	72.8	411	თ	Q9TU02	oryc
æ	1761.5	70.6	431	11	Q9R1A7	Q9rla7 rattus norv
9	1753.5	70.3	342	4	Q9UJ22	
10	991.5	39.8	386	13	Q91839	Q91839 xenop
11	817	32.8	420	13	Q91B73	Q91b73 paralichthy
12	796	31.9	453	13	Q9PTN2	Q9ptn2 brachydanio
13	790.5	31.7	425	13	Q9IB74	Q91b74 paralichthy
14	729	29.2	358	11	Q9QUS1	Q9qus1 rattus norv
15	504.5	20.2	445	11	Q9QUH7	Q9quh7 mus musculu
16	500.5	20.1	455	4	Q12970	Q12970 homo sapien
17	472.5	18.9	472	4	Q92943	Q92943 homo sapien
18	463	18.6	469	11	Q62735	
19	460		200			Q62735 rattus norv

Query Match 100.0%; Score 2494; DB 4; Length 473; Best Local Similarity 100.0%; Pred. No. 3.7e-204; Matches 473; Conservative 0; Mismatches 0; Indels 0

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Gaps

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Receptor. SEQUENCE 473 AA; 53899 MW; 3049D23C9B903016 CRC64;	; PS00031;	PRINTS: PRO0398: STRDHORMONER.	PR00047;	F00105; zf	PF00104;			IPR000536;	TATERDED: TERRONOSZA: -		Proc. Natl. Acad. Sci. U.S.A. 95:12208-12213(1998).	induction.";	"Identification of a human nuclear receptor defines a new signaling	Berkenstam A.;	stlind H., Blomquist P.,	Bertilsson G., Heidrich J., Svensson K., Asman M., Jendeberg L.,	MEDLINE-98445350; PubMed-9770465;	IVER:	SEQUENCE FROM N.A.			'Primates: Catarrhini: Hominidae:	Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:		m	(TrEMBLrel. 15, Last annotation	(TrEMBLrel. 13,	(TrEMBLrel.		Q9UW4 PRELIMINARY; PRT; 473 AA.	TOTAL +		

Best Local Similarity 98.4 Matches 442; Conservative

98.4%;

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HSSP; P10826; 1HRA.
INTERPRO; IPR000324; -
INTERPRO; IPR000536; -
INTERPRO; IPR001628; -
INTERPRO; IPR001723; -
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                                                                   Receptor.
SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Heard D.J., Holloway J.,
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                                                                                                           PS00031;
                                                                      457
                                                                                                                                                                                                                                                                                                                                                                                     Genet.
                                                                   AA;
                                                                                                                                  ; STROIDFINGER.; VITAMINDR.; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBLrel. 13, Created)
EMBLrel. 13, Last sequence update)
EMBLrel. 15, Last annotation update)
RECEPTOR PRR1-C.
                                                                                                             NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                       . 0:0-0(0).
                                                                 52145 MW;
  93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hansen
  Score
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                                                               812F8B354B5B784E CRC64;
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  2330;
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4
Length
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3q12.1
457;
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HSSP; P10826; 1HRA.
INTERPRO; IPR000324; -.
INTERPRO; IPR000536; -.
INTERPRO; IPR001528; -.
INTERPRO; IPR001723; -.
                                                               PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00356; VITAMINDR.
PRINTS; PR00338; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LIVER;
Heard D.J., Holloway
Vissing H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Meta::oa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                    -13.3.";
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01-OCT-2000
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    SEQUENCE
                     Receptor
                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                Eur. J. Hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
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(TrimBLrel. 13, Last sequence update)
(TrimBLrel. 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                Genet.
ÃĄ;
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                                           NUCLEAR_RECEPTOR;
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  49777 MW;
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AB36DEC23C4C4200 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                               nuclear
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Best Local S
Matches 431
INTERPRO; IPRO00324; -.

R INTERPRO; IPRO00324; -.

R INTERPRO; IPRO00536; -.

R INTERPRO; IPRO01528; -.

R INTERPRO; IPRO01723; -.

R INTERPRO; IPRO01723; -.

PFAM; PF00104; hormone_rec; 1.

PFAM; PF00105; zf-C4; 1.

PFAM; PF00105; zf-C4; 1.

PFAM; PF00105; zf-C4; 1.

PFAM; PF00105; zf-C4; 1.

PFINTS; PR00350; VITAMINDR.

PRINTS; PR00398; STROHORMONER.

PRINTS; PR00398; STROHORMONER.

PRINTS; PR00346; THYROIDHORMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UJ23
Q9UJ23;
Q1-MAY-2000
Q1-MAY-2000
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-LIVER;
Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard Vissing H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                 normone receptor PXR/SXR and
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR HORMONE
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                                                                                                                                                                                                                                                               AJ009937; CAE
P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 99.3
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence up
(TrEMBLrel. 15, Last annotation
MONE RECEPTOR PRR2-C.
                                                                                                                                                                                                                                                                               . Genet. 0:0-0
937; CAB55493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                      . 0:0-0(0).
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                                                                                                                                                                                                                                                                                                                                                                        novel
                                                                                                                                                                                                                                                                                                                                                   protein isoform of the human nd localization to chromosome
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Pred. No. 8.1e-186;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                        chromosome 3q12
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Best Local S
Matches 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UJ24

Q9UJ24;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
01-OCT-2000 RECEPTOR PRR2-A.
                                            HSSP: AJ009937; CAB55492.
HSSP: D10826; 1HRA.
INTERPRO; IPR000324; -.
INTERPRO; IPR000536; -.
INTERPRO; IPR001628; -.
INTERPRO; IPR001723; -.
INTERPRO; IPR001728; -.
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SEQUENCE 420 AA; 48149 MW; CF4D9
                                                                                                                                                                                                                                               TISSUE-LIVER:
Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard
Vissing H.:
"Identification of a novel protein isoform of the human
hormone receptor PXR/SXR and localization to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRR2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                  Eur. J.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392
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                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
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405; Conserv
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nilarity 90.2%;
Conservative
                                                                                                                                                                                                                  Genet.
  hormone_rec;
zf-C4; 1.
                                                                                                                                                                                           CAB55492.1;
                                                                                                                                                                                      0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.4e-171;
); Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF4D9E1256859165 CRC64;
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                                                                                                                                                                                                                                                                                                                                   Tommerup N., Aagaard
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3q12.1
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Q90J25;
                                                             EMBL;
HSSP;
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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SEQUENCE
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                                           INTERPRO;
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Local Similarity
                                                                                               J. Hum. Genet.
                                                           AJ009936;
P10826; 1H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATPLMQELFGITGS 473
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PR00398; S
PR00546; I
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9930,
826; 1HRA.
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                                                                                                                                                                                           Holloway
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STRDHORMONER.
THYROIDHORMR.
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Primates;
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Pred. No. 3.5e-167;
                                                                                                                                     localization
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Best Local Sin
Matches 378;
MEDIINE-20092326; PubMed-10628745;
Jones S.A., Moore L.B., Shenk J.L., Wisely
McKee D.D., "Tomkinson N.C., LeCluyse E.L.,
Kliewer S.A., Moore J.T.;
"The pregnane X.receptor: a promiscuous xe
diverged during evolution.";
Mol. Endocrinol: 14:27-39(2000).
EMBL; AF182217; AAD54426.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                         STRAIN-BREED NEW ZEALAND WHITE RABBIT; TISSUE-KIDNEY; Savas U., Wester M.R., Griffin K.J., Johnson E.F.; Savas U., Wester M.R., Griffin K.J., Johnson E.F.; "The rabbit pregnane x receptor is activated by rifampicin."; submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREGNANE X RECEPTOR.
NR112 OR PXR.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-04; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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99.7%;
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Pred. No. 6.2e-160;
0; Mismatches 1;
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                                                                                                                                                          Wisely
e E.L.,
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                                                                                                         xenobiotic receptor that
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                                                                                                                                                          G.B., Hamilton
Lambert M.H., 1
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Best Local Similarity 83.1%;
Matches 339; Conservative 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO, IPRO00334; -.
INTERPRO; IPRO00536; -.
INTERPRO; IPRO01528; -.
INTERPRO; IPRO01723; -.
INTERPRO; IPRO01723; -.
PFAM; PF00105; Zf-C4; 1.
PFAM; PF00105; Zf-C4; 1.
PFAM; PF00047; STROIDPINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00351; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          O9RIA7 PRELIMINARY;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-OCT 2000 (TrEMBLrel. 1
PREGNANE X RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                            INTERPRO;
                                                                                                STRAIN-SPRAGUE-DAWLEY;
Zhang H., LeCulyse E., Liu L., Hu M., Matone;
Zhang H., LeCulyse E., Liu L., Hu M., Matone;
"Rat Pregnane X Receptor: Molecular Cloning,
Xenobiotic Regulation.";
Xenobiotic Regulation.";
Arch. Biochem. Biophys. 368:14-22(1999).
Arch. Biochem. Biophys. 368:14-22(1999).
EMBL AFISI377; ADA47214.1; -.
HSSP; P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P10826; 1HRA.
INTERPRO; IPR000324;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                        INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLLEPML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELGTMKLSLQLRGEDGSVWNYTPPADRSGKKLFSLLPHLADMSTYMFKGIINFAKVISYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFHYMLKKLQLHKEEYVLMQAISLFSPDRPGVVQREVVDQLQERFAITLKAYIECSRPQP
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IPR000324; -. IPR000536; -. IPR001628; -. IPR001723; -.
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13,
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Last sequence update)
Last annotation updat
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Pred. No. 2.2e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BBF955EC17E2E71A CRC64;
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                                                                                                                                                                                                  Matoney L., Zhu W., Yan B.;
loning, Tissue Distribution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; DB 6;
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Best Local :
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Q9UJ22;
01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor.
SEQUENCE
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PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
      Eur. J. Hum. Genet. 0:0-0(0
EMBL; AJ009937; CAB55494.1;
HSSP; P10826; 1HRA.
INTERPRO; IPR000324; -.
                                         hormone receptor PXR/SXR and locali
                                                                      Heard D.J.,
Vissing H.;
                                                                                                                    NCBI_TaxID=9606;
                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                    NUCLEAR HORMONE
                                                                                          TISSUE-LIVER
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   462
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                                                                                                                                                                                                                                                                                                              DQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFAT
                                                                                                                                                                                                                                                                                                                                         RLAYCFEDPNGGFQKLLLDPLMKFHCMLKKLQLREEEYVLMQAISLFSPDRPGVVQRSVV
                                                                                                                                                                                                                                                                                                                                                 RLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRPEERWNHVGLVQREEADSVLEEP-INVDEEDGGLQICRVCGDKANGYHFNVMTCEGCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 AA; 49660 MW;
                                                                                                                                                                          (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 15, Last annotation
                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                               Holloway
                                                                                                                                                                                                                                                                                  471
                                                                                                                                                                     RECEPTOR
                                                                                                                              Chordata;
Primates;
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                                                                                                                                                                     PRR2-B.
                                                                                 Hansen
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Pred.
                                                      localization
                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4B545F21F9439697 CRC64;
                                                                              c.,
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No. 7.46
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                                                                               Tommerup N., Aagaard
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nes 57;
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                                                                                                                                                                                    update)
                                                              of the human
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                                                      chromosome
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3q12.1
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PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; ST-COIDFINGER.
PRINTS; PR00350; VITAMINUR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00346; THYROIDHORMR.
EMBL; X75163; CAA53006.1; -.
HSSP; P10826; 1HRA.
INTERPRO; IPR000536; -.
INTERPRO; IPR001628; -.
PFAM; PF00104; hormone_rec; 1
PFAM; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                   Q91839;
Q91839;
                                                                      SEQUENCE FROM N.A.

MEDLINE-94173664; PubMed-8127656;

MEDLINE-94173664; PubMed-8127656;

Smith D.P., Mason C.S., Jones E.A., Old R.W.;

"A novel nuclear receptor superfamily member in xenopus that associates with RXR, and shares extensive sequence similarity mammalian vitamin D3 receptor.";

Nucleic Acids Res. 22:66-71(1994).

EMBL; X75163; CAA53006.1; -.
                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 13, Last sequence update)
01-NOV-1996 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
0RPHAN NUCLEAR RECEPTOR OF STEROID/THYROID SUPERFAMILY.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Pipoidea; Pipidae;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPRO01628; -.
INTERPRO; IPRO01723; -.
INTERPRO; IPRO01728; -.
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Pred. No. 2.6
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68 VNADE-EVGGPQICRVCGDKATGYHENVMTCEGCKGFFRRAMKRNARLRCPFRKGACEIT 126

VGPDEFDRNAPRICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKASFTCPF-NGSCTIT

Query Match Best Local S Matches 179

Similarity

32.8%;

Conservative

70;

Score 817; DB Pred. No. 1.8e

DB 13; .8e-61;

Length

420;

Indels

22;

Gaps

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01-0CT-2000
01-0CT-2000
                                                                                                                                  Paralichthys olivaceus (Flounder).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Bothidae; Paralichthys.

NCBI_TaxID-8255;
 SUZUKI T., SUZUKI N., STIVASTAVA A.S., KUTOKAWA "Identification of cDNAS encoding two subtypes of Inflounder, Parallchthys ollvaceus.";
Biochem. Biophys. Res. Commun. 270:40-45(2000).
EMBL; AB037674; BAA95016.1; -
Receptor.
Receptor. 420 AA; 47486 MW; 038FBF00D4F38067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0047; STROIDEINGER.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
SEQUENCE 386 AA; 44302 MW; 8B04
                                                                                            TISSUE-INTESTINE;
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                               VITAMIN D RECEPȚOR A.
                                                                                                                                                                                                                                                                                      Q9IB73;
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                                                                                                                                                                                                                                                                                                                                                                                  415 YIECNR-PQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFG
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420 AA;
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Pred.
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8B046ED219556573
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                                                                     Of 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00047; STROIDFINGER. PRINTS; PR00350; VITAMINDR. PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Danio rerio vitamin D receptor.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF166512; AAF21427.1;
HSSP; P20393; 1A6Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kouzmenko A.P.
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155 EAVEERRALIKRKKSE---RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNF 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 CNRPQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG 469
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                                                                                                                                                                                 GGKSKCEAGACESTVNGDATSLMDLMAVSTSATGQDQFDRNAPPICGVCGDKATGFHFNA 70
                                                                  MTCEGCKGFFRRSMKRKASFTCPF-NGNCTITKDNRRHCQACRLKRCIDIGMMKEFILTD 129
                                                                                                              MTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACKLRKCLESGMKKEMIMSD 154
                                                                                                                                                                                                                                          GPEANLEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNV 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00104; hormone_rec; 1. PF00105; zf-C4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 AA;
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              50765 MW; B52C82C185859F9C CRC64;
                                                                                                                                                                                                                                                                                                   31.9%; Score 796; DB 13; 39.7%; Pred. No. 1.2e-59; tive 76; Mismatches 165;
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Last sequence update)
Last annotation update)
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Q9IB74;
Q9IB74;
Q1-OCT-2000 (TrembLrel. 15; Created)
Q1-OCT-2000 (TrembLrel. 15; Last sequence update)
Q1-OCT-2000 (TrembLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki T., Suzuki N., Srivastava A.S., Kurokawa T.; "Identification of cDNAs encoding two subtypes of v In flounder, Paralichthys olivaceus."; Biochem. Biophys: Res. Commun. 270:40-45(2000). EMBL, AB037673; BAA95015.1; -
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                                       286
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                       STYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGR--L
                                                                                  LSDASSDSFSHSPESV-DTKVNFNNLLMMYQEQGS----SPDSSEEEGSSFSMLPHLADL
                                                                                                                                                    PSREEAAKWSQVRKDLCSLKVS----LQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADM
                                                                                                                                                                                                                                                                        GTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSSGCELPESLQA
                                                                                                                                                                                                                                                                                                                                          NGSCTITKDNRRHCQACRLKRCVDIGMMREFILTDEEVQRKKDLIQRRKDEEAQREAERE 122
                                                                                                                                                                                                                                                                                                                                                                                                     KGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKK-----SERT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVPGKPSVNADE-EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVVSTSSLASDEFDRNMPRICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKATFTCPF-
                                                                                                                                                                                                                ARRP----RLTDEQSQVIAMLVEAHHKTYDDSYSDFCRFRPPVREGPVTRSASRAASLHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%; Score 790.5; DB 1
41.6%; Pred. No. 3.3e-59;
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Best Local
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                         PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PFANTS; PR00047; STROIDEINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00546; THYROIDHORMR.
                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPRO00324; -.
INTERPRO; IPRO00536; -.
INTERPRO; IPRO01628; -.
INTERPRO; IPRO01723; -.
INTERPRO; IPRO01728; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9QUS1
Q9QUS1;
01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshinari K., Sueyoshi T., Moore R., Negishi M.;
Sexually dimorphic nuclear translocation of receptor CAI
induction of CYP2B1 gene by phenobarbital in rat livers.
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133095; AAF22567.1;
EMBL; AF133094; AAF22566.1;
HSSP; P19793; ZNLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-WISTAR KYOTO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                            PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
                                                                                                                           132 QCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPIGVQGLTEEQRMMIR
164
                         252
                                                                              192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                       72 EEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALQDRLSETLQAYIQLH--HPGGRLLYAKMIQKLADLRSLNEEHSKQYRSLSFRPEHSMQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLOEOFAITLKSYIECNRPOPAHRFLFLKIMAMLTELRSINAOHTO--RLLRIQDIHPF- 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYQISDVTKAGHTLELLEPLVKFQVGLKKLNIQEEEHVMLMAICLLSPDRPGVQDHARIE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVD 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSYSIQKVIGFAKMIPGFRELTAEDQIALLKSSAIEVIMLRSNQSFNLEDMSWSCGAPDF 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTPLVLEVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPLMQELFG
                                                                                                       HCPACRLQKCLNVGMRKDMILSAEALALRRARQARRRAQKASLQ------LSQQQKELIQ 125
                                                                                                                                                             TLLGAHTRHVGPMFDQFVQFRPPAYLFSH-HRPFQPLAP-----
                                                                            ELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVS
                         LQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQ 311
                                                                                                                                                                                                                  160;
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                    358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                    A
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469
                                                                                                                                                                                                                                                                                    40922 MW; 13691F49CAD8F1ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND FISCHER;
                                                                                                                                                                                                                29.2%; Score 729; DB 11;
40.3%; Pred. No. 4.5e-54;
tive 61; Mismatches 122
 -VLPLLTHFADINTFMVQQIIKFTKDLPLFRSLTMEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rat livers.";
                                                                                                                                                                                                                                           Length 358;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                    Gaps
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                                                        163
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SOURCE PROPERTY OF THE PROPERT
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Best Local Sin
Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00104; hormone_rec; 1.

PFAM; PF00105; zf-c4; 1.

PRINTS; PR00047; STROIDFINGER.

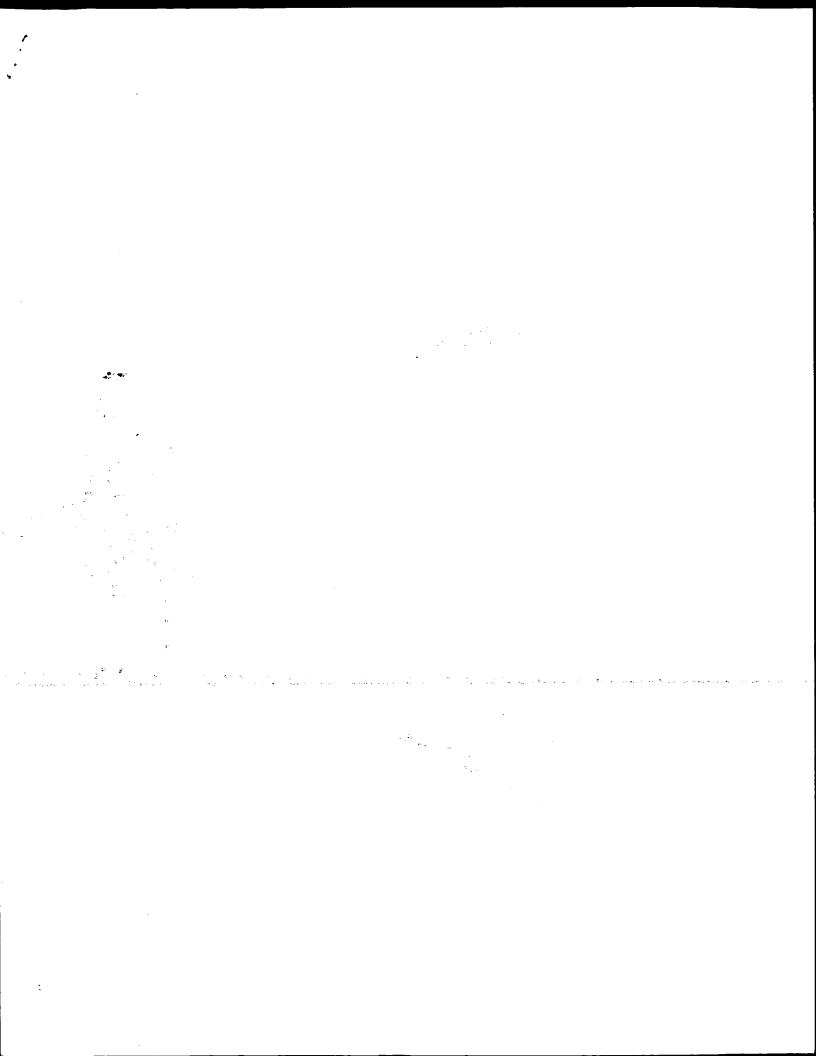
PRINTS; PR00350; VITAMINDR.

PRINTS; PR00398; STRDHORMONER.

PRINTS; PR00346; THYROIDHORMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO00324; ...
INTERPRO; IPRO00336; ...
INTERPRO; IPRO00923; ...
INTERPRO; IPRO01628; ...
INTERPRO; IPRO01723; ...
INTERPRO; IPRO01728; ...
INTERPRO; IPRO03069; ...
INTERPRO; IPRO03078; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QUH7 PRELIMINARY; PRT; 445 AA.
Q9QUH7;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NUCLEAR OXYSTEROL RECEPTOR LXR-ALPHA (LXR-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132599; CAB51952.1; -.
EMBL; AJ132600; CAB51992.1; JOINED.
EMBL; AJ132601; CAB51923.1; -.
HSSP; P20393; 1A6Y.
HSSP; P20393; 1A6Y.
MGD; MGI:1352462; Nr1h3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-129SVJ; TISSUE-LIVER, Alberti S., Steffensen K.R., G "Cloning and characterisation and LXRb from mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NR1H3 OR LXR-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1283; ECDYSTEROLDR.
PRINTS; PR01292; RETNOICACIDR.
PROSITE; PS00031; NUCLEAR RECE
PROSITE; PS00196; COPPER_BLUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 KIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQEL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                       73
                                                                                                                                   ISLLKGAAFELCOLRENTVFNAETGTWECGRLSYCLEDTAG-GFQQLLLEPMLKFHYMLK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISLLKGAAVEILHISLNTTFCLQTQNFFCGPLCYKMEDAVHVGFQYEFLELIIHFHKTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLMGLLAELRSINSAYSYEIHRIQGLSAM-MPLLGEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIQIQEPEYALMAAMALESPDRPGVTQREEIDQIQEEVALIINNHIMEQQSRIQSRFIYA
                                               PFRKGACEITRKTRRQCQACKLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 170
                                                                                                       -HSGGHCPMDJYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAQATS 189
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                     445
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                  ΛA;
                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR_RECEPTOR; 1.
COPPER_BLUE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                     50476 MW;
                                                                                                                                                                                                               20.2%; Score 504.5; 30.4%; Pred. No. 7.86; ive 85; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gustafsson J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                        CC9A8DF38D935593 CRC64;
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                                                                                                                                                                                                                                                7.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxysterol receptor
                                                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                          142;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                          Length 445;
                                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes LXRa
                                                                                                                                                                                                                          Gaps
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	-		436 LISETUV 443	7.7	3
		70	463 LMQELFGI 470	463	δ
43	OVFALRIQDKKLPP	380 QHTYVEALHAYVSINHPHDRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQDKKLPP 43:	QHTYVEALHAI	380	망
46	RLLRIQDIHPFATP	405 QEQFAITLKSYIECURPQPAHRELELKIMAMLTELRSINAQHTQRLLRIQDIHPFATP 46	QEQFAITLKS1	405	Ş
379	SADRPNVQDQLQVERL	320 NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL 37	NREDFAKAGL	320	문
ç Q	SPDRPGVLQHRVVDQL	346 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEXYLMQAISLFSPDRPGVLQHRVVDQL 404	CLEDTA-GGE	346	γQ
319	NPGSESITE-LKDFSY	261 VSVQETVDFAKQLPGFLQLSREDQTALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY 31:	VSVQEIVDFA	261	망
34	NAETGTWECGRLSY	288 YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSY 34:	YMFKGIISFA	288	Ş
260	ARQQREAHFTELAI	229DRLRVTPW-PIAPD	DRLRVTP	229	밁
287	SKEIFSLLPHMADMST	228 QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 28	QAPSREEAAKI	228	οy
228		190 VSPRVSSPPQVLPQLSPEQLGMIEKLVAAQQQCNRRSFS 228	VSPRVSSPPQ	190	밁
227	RLPGVLSSGCELPESL	171RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESL 22:	RTGTQPL	171	ρ

Search completed: February 18, 2001, 13:05:05 Job time: 6194 sec



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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match
  US-09-143-828-4
2494
1 MTVTRTHHEKEGSLRAPAIP.....QDIHPFATPLMQELFGITGS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               February 18, 2001, 13:43:38; Search time 51.75 Seconds (without alignments)
295.171 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88757 seqs, 32294092 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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PXR_HUMAN
PXR_WOUSE
PXR_RAT
PXR_RAT
VDR_COTJA
VDR_COTJA
VDR_COTJA
VDR_BOVIN
VDR_HUMAN
NRII3_HUMAN
NRII3_HUMAN
NRII3_HOMAN
NRII3_HUMAN
NRII3_HOMAN
THB_CHICK
THB_CHICK
THB_CHICK
THB_CHICK
THB_ANCIA
THBL_HUMAN
THBL_HUMAN
THBL_HUMAN
THBL_RAT
THBB_ZENIA
THBB_ZENIA
THBB_ZHOMAN
THBL_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
 P48281 mus musculu
Q28037 bos taurus
P11473 homo sapien
O14994 homo sapien
O9qusi rattus norv
O35627 mus musculu
P5055 homo sapien
Q9209 mus musculu
O52685 rattus norv
Q13133 homo sapien
Q60644 mus musculu
O62755 rattus norv
Q13137 homo sapien
P37845 ratus norv
O18531 lucilia cup
O91279 paralichthy
P49880 aedes aegyp
P10828 homo sapien
P18112 gallus gall
O02965 rana catesb
P18113 rattus norv
P37244 mus musculu
P18114 renopus lae
P18115 ratus norv
P37826 rattus norv
P37826 rattus norv
                                                                                                                                                                                                                                                                                                                                                                       075469 homo sapien
054915 mus musculu
Q9r1a7 rattus norv
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11 lucilia cup
9 paralichthy
10 acdes acyp
10 acdes acyp
10 homo saplen
2 gallus gall
15 rana catesb
7 xenopus lae
2 homo saplen
2 mus musculu
9 xenopus lae
3 rattus norv
4 mus musculu
15 homo saplen
6 rattus norv
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1 coturnix co
2 gallus gall
4 xenopus lae
3 rattus norv
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ROT e Swis Biol Biol Biol Chires this this this this this this this thi	350; Me Me Min Min Min Min Min Min Min Min	STAN 11. 3 11. 3 RECE LUMAN LOGA; PIA: 10. 3 RECE RECE RECE RECE RECE RECE RECE REC	17.5 17.44 17.44 17.11 17.0 17.0
ntry is copyrig s Institute of nformatics Inst it institution it institution statement is n a license agre to license@isb to license@isb AD05436.1; AC64558.1; AC64558.1;	N.A. Heidrich J., Heidrich J., M., Ohlsson R. n of a human r. p3a induction. ad. Sci. U.S. ORPHAN RECEPTO ORPHAN RECEPTO ORMS A HETEROL BINDS TO A RES BINDS TO A RES BINDS TO EXPL ORMS A HETEROL ENTER YEAR BELORGS TO J. ELLY.	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	54445545455455 5444556 544456 54456 54456 5446 546 5
cop tute ics titute titute titute nse nse nse nse 1.1;	Med-97704 .ch J., Sv .sson R., human nuc luction."; U.S.A. RECEPTOR; O A RESPO O A RESPO IN NUCLION: N	ערות שים אוו אוו אוו אוו	
It is produced informatics and the There are no is long as its or removed. Usage ant (See http://www.ch).	Svensson K., Asman M., Jo , Postlind H., Blomquist , Postlind H., Blomquist , Postlind H., Blomquist , Postlind H., Blomquist , Postlind Teceptor defines (, Postlind Teceptor In Ingano IS , Ponse Element In THE CYP. DIMER WITH RXR. DIMER WITH RXR. DESSED IN LIVER, COLON, ALLESSED IN LIVER, COLO	PRT; 434 AA. d) equence update) nnotation update) (PREGNANE X RECEPTOR) (OI ; Craniata; Vertebrata; I ; Catarrhini; Hominidae; ; Catarrhini; Hominidae; 7070; tson M.A., Willson T.M., ceptor PXR is activated I sion and cause drug inter 23(1998).	THA1_BRARE ECR_DROME THAA_PAROL ECR_MANSE RCR_HUMAN RORG_HUMAN RRA_XENLA RRA_YENLA RRA_CHICK RRB_CHICK RRB_CHICK THB1_SHEEP ECR_CHITE ALIGNMENTS
ough a collaborati e EMBL outstation restrictions on i ent is in no w and for commerci isb-sib.ch/announc	y Jendeberg L., ist P., ist P., is probably CYP3A4 GENE PROMOTER. , AND SMALL TEROIDS SUCH AS CEPTORS FAMILY.	(ORPHAN NUCLEAR; Euteleostom1; e; Homo.	Q98867 brachydanio P34021 dxosophila Q91241 paralichthy P49883 manduca sex P10826 homo sapien P51149 homo sapien P51126 xenopus lae Q60674 mus musculu P04625 gallus gall P22448 gallus gall P23871 ovis aries P49882 chironomus

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RESULT 2
PXR_MOUSE
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Best Local Similarity
                                                                                                 PXR_MOUSE STANDAKU;

054915;

054915;

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

01-OCT-2001 (Rel. 40, Last annotation update)
          Kliewer
Jones S.
                                                                            NRIIZ OR PXR.
Mus musculus (Mouse).
Eukaryota; Metazoa; C
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DOMAIN
SEQUENCE
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ZN_FING
ZN_FING
                             MEDLINE=98149345; PubMed=9489701;
                                         TISSUE-LIVER;
                                                 SEQUENCE FROM N.A.,
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PFAM; PF00105; zf-c4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINUR.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Transcription regulation; Zinc-finger.
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                                                                                                                                                                                                                                                                                                                                    PHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWE
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                                                                                                                                                                                                                                                                                                                                                                                       GCELPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLL
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          S.A., McKee
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          Moore
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77
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                                                                   Chordata;
Rodentia;
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61
102
204
434
          J.T., Wade
.D., Oliver
                                                AND ALTERNATIVE
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99.8%;
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C4-TYPE.
C4-TYPE.
HINGE.
HINGE.
LIGAND-BINDING.
LIGAND-BINDING.
TDF6A2AE3109C4DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2287; DB 1;
Pred. No. 6.9e-176;
1; Mismatches 0;
                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
          B F
        Staudinger J.L.,
., Willson T.M.,

    DNA-binding; Nuclear protein;

                                                 SPLICING
                                                                               Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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        Zetterstrom
                 Watson
                                                                    Murinae;
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A.A.,
Tom R.H.,
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Best Local S
Matches 332
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ZN_FING
ZN_FING
DOMAIN
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SEQUENCE
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INTERPRO; IPR000324; -.
INTERPRO; IPR000336; -.
INTERPRO; IPR001638; -.
INTERPRO; IPR001723; -.
INTERPRO; IPR001723; -.
IPAM; PF00104; 'hormone_rec; 1.
PFAM; PF00104; 'hormone_rec; 1.
PFAM; PF00105; zf-c4; 1.
PRINTS; PR0015; zf-c4; 1.
PRINTS; PR00047; STROHOFINGER.
PRINTS; PR00398; STROHOMNOR.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION INGLIAR_NECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREGNANE. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTISTS OF A RESPONSE ELEMENT IN CYP3A GENES PROMOTISTS OF A RESPONSE ELEMENT IN CYP3A GENES PROMOTISTS OF A HETERODIMER WITH RXR.

1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PXR.1 (SHOWN HERE) AND 2/PXR.2; AR3 PRODUCED BY ALTERNATIVE SPLICING.

1- INDUCTION: ACTIVATED BY NATURALLY OCCURRING STEROIDS SUCH A PREGNENOLONY AND PROGESTERONE, SYNTHETIC GLUCOCORTICOIDS AND 16-ALPHA-CARBONITRILE (PCN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF031814; AAC39964.1; MGD; MGI:1337040; NR112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            steroid signaling pathway.";
Cell 92:73-82(1998).
                    342
                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "An orphan nuclear receptor activated by pregnanes defines a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perlmann T., Lehmann J.M.;
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 77.2
nes 332; Conservative
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                                                                                                                                                                                                                                                                                                                     1 MRPEESWSRVGLVQCEEADSALEEP-INVEEEDGGLQICRVCGDKANGYHFNVMTCEGCK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY NR1 SUBFAMILY.
RLSYCLEDTAGGEQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLESPDRPGVLQHRVV
                                                                     MADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECG
                                                                                                                                                                                                                                                     GFFRRAMKRNYRLRCPFRKGTCEITRKTRRQCQACRLRKCLESGMKKEMIMSDAAVEQRR 119
                                                                                                                                                                                   ALIKRKKREKIEAPPPGGGGLTEEQQALIQELMDAQMQTFDTTFSHFKDERLPAVFHSGC
                                                                                                                                                                                                      ALIKRKKSER@GTQPLGVQGLTEEQRAMIRELADAQAKTFDTTFSHFKNFRLPGVLSSGC
                                                                                                                                                                                                                                                                      GFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERR 161
                                                   LADVSTYMFKGVINFAKVISYFRDLPIEDQISLLKGATFEMCILRFNTMFDTETGTWECG
                                                                                                                                     ELPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPH
                                                                                                                   ELPEFLQASLLEDPATWSQIMKDRVPMKISLQLRGEDGSIWNYQPPSKSDGKEIIPLLPH
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38 104 C4-TYP
38 58 C4-TYP
74 99 C4-TYP
105 201 HINGE.
202 431 LIGAND
171 211 MISSIN
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77.28;
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Pred. No. 3.1e
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINGE.
LIGAND-BINDING.
MISSING (IN ISOFORM
F592AF91F689329E (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4-TYPE ZINC
C4-TYPE.
C4-TYPE.
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e-135;
55;
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01-OCT-2000 (Rel. 40, Createu)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
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Q9R1A7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang H., LeCulyse E., Liu L., Hu M., Matoney
"Rat pregnane X receptor: molecular cloning,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECE
                                                                                                                                                                                                                                                                           PFAM; PF00104; hormone_rec; 1. PFAM; PF00105; zf-C4; 1. PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF151377; AAD47214.1;
                                                                                                                                DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO;
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SUBUNIT: FORMS A HETERODIMER WITH
SUBCELLULAR LOCATION: NUCLEAR (BY
SIMILARITY: BELONGS TO THE NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLMQELFSST 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLMQELFGIT
                                                                                                                                                                                                                                                                                                                                                                                                    IPR000324; -. IPR000536; -.
                                                                                                                                                                                                                                                                                                                                                    IPR001628; -. IPR001723; -.
                                                                                                                                                                             Transcription
                                                                            38
74
     ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                       NUCLEAR_RECEPTOR;
  49660
                                                                                                                                                                             regulation; DNA-binding; Nuclear protein;
  WW;
                    C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
C4-TYPE.
HINCE.
LIGAND-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR
  4B545F21F9439697 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matoney L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhu W., Yan B.;
ie distribution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLY
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2

Query Match Best Local S Matches 330

Similarity

70.6%; 76.7%;

Score 1761.5; Pred. No. 8.46

DB 1;

431; 1.

330;

Conservative

42;

Mismatches

es 57;

Indels Length

Gaps

HSSP;

U12641; AAA56725.1; P03372; 1HCQ.

IPR000324;

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VDR_COTJA
P49701;
01-FEB-1996 (
01-FEB-1996 (
30-MAY-2000 (
VITAMIN D3 RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metażoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasian
                                                                                                                                                                                                                                                                                                                                                                          TISSUE-CHORIOALLANTOIC MEMBRANE;
MEDLINE-95062315; Pubmed-7972109;
Elaroussi M.A., 'Prahl J.M., Deluca
"The avian vitamin D receptors: pri
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDR OR NR111.
                                                                                                                                                                                                                                                                                                                                                           origins
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                                                                                                                                                                                                                                                                                                                                            Proc.
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                                                                                                                                                                                                         C. NATI. ACAD. SCI. U.S.A. 91:11596-11600(1994).

C. NATI. ACAD. SCI. U.S.A. 91:11596-11600(1994).

C. NATI. CONTROLLING THE ACTION OF VITAMIN D3 BY CONTROLLING THE EXPRESSION OF HORMONE SENSITIVE GENES.

SUBCELLULAR. LOCATION: NOCLEAR.

ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED BY USE ALTERNATIVE: INITIATION CODONS IN THE SAME READING FRAME. ALTERNATIVE: INITIATION CODONS IN THE SAME READING TRAME.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING NOTERNINAL DO A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLESPDRPGVLQHRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRPEERWNHVGLVQREEADSVLEEP-INVDEEDGGLQICRVCGDKANGYHFNVMTCEGCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLMQELFSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLMQELFGIT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LADVSTYMFKGVINFAKVISHFRELPIEDQISLLKGATFEMCILRFNTMFDTETGTWECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELPEVIQASLLEDPATWSQIMKDSVPMKISVQLRGEDGSIWNYQPPSKSDGKEIIPLLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFFRRAMKRN VRLRCPFRKGTCEITRKTRRQCQACRLRKCLESGMKKEMIMSDAAVEQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLAYCFEDPNGGFQKLLLDPLMKFHCMLKKLQLREEEYVLMQAISLFSPDRPGVVQRSVV
                                                                                                                                                                                                 SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (Rel. 33, Created)
6 (Rel. 33, Last sequence update)
0 (Rel. 39, Last annotation update)
0 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ȘTANDARD;
                                                                                                                                                                                                                                                                                                                                                                          receptors: primary
                                                                                                                                                                                                                                                                                                                                                                                         H.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D3 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                             and their
                                                                                                                                                                                                                                                                                                                              BY CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostom1;
                                                                                                                                restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phasianinae;
                                                                                                                                                 collaboration
                                                                                                                                                outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sim
Matches 179;
                                                                                                                                                  VDR_CHICK
042392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
SEQUENCE
                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INIT_MET
DNA_BIND
ZN_FING
ZN_FING
              STRAIN-LEGHORN;
                         SEQUENCE
                                                         Archosauria;
                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00031; NUCLEAR_RECEPTOR; Receptor; Transcription regulation; Zinc-finger; Alternative initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00104; hormone_rec; PFAM; PF00105; zf-C4; 1.
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                                                                                                                                                                                    u
                                                                                                                                                                                                                                                                                                                                                        MLPHLADLVSYSIQKVIGFAKMIPGFRDLTAEDQIALLKSSAIEVIMLRSNQSFTMEDMS
                                                                                                                                                                                                                     FOREHSMOLTPLVLEVFG 444
                                                                                                                                                                                                                                                                                                                         WECGR--LSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CESQELQSSDMETPAVGTPEFDRNVPRICGVCGDRATGFHFNAMTCEGCKGFFRRSMKRK 75
                                                                                                                                                                                                                                           IQDIHPF-ATPLMQELFG 469
                                                                                                                                                                                                                                                                 VQDTSLVESIQDRLSDTLQTYIRCRHPPPGSRLLYAKMIQKLADLRSLNEEHSKQYRCLS
                                                                                                                                                                                                                                                                                     VLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLR
                                                                                                                                                                                                                                                                                                             WTCGSNDFKYKVSDVTQAGHSMDLLEPLVKFQVGLKKLNLHEEEHVLLMAICILSPDRPG
                                                                                                                                                                                                                                                                                                                                                                               LLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGT
                                                                                                                                                                                                                                                                                                                                                                                                      SQDFSSEDSNDVFGSDAFGAFPEPMEPQMFSNLDLSEESDESPSMNIELPH-----LP
                                                                                                                                                                                                                                                                                                                                                                                                                            SSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSER
                                                                              gallus (Chicken).
                                                                                             NR1I1.
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                       FROM
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26
44
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110
213
                                                         Aves; Neognathae;
N.A.
N; TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
448
109
109
104
104
212
                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 815.5; DB 1;
Pred. No. 5.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FCF1FC3DEAEEAF3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VITAMIN D3
VITAMIN D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOR ISOFORM B.
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Nuclear protein;
                                                                                                                                                             451
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                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOFORM
ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                    Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 235:1214-1217(1987).

-I- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D
-IHE EXPRESSION OF HORMONE SENSITIVE GENES.

-I- SUBCELLULAR LOCATION: NUCLEAR.

-I- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF011356; AAB62579.1; INTERPRO; IPR000324; -. INTERPRO; IPR000536; -. INTERPRO; IPR001628; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE: INITIATION CODONS.

1 TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.

1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN: A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Malley B.W.; "Molecular cloning of complementary DNA encoding the for vitamin D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lu Z., Hanson K., Deluca H.F.; "Cloning and origin of the two forms of chicken vitamin Arch. Biochem. Biophys. 339:99-106(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87149040; PubMed-3029866; McDonnell D.P., Mangelsdorf D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 45-114 FROM N.A.
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                                                                                                                                                                                  CEGCKGFFRRSMKRKAMFTCPF-NGDCKITKDNRRHCQACRLKRCVDIGMMKEFILTDEE
                                                                                                                                                                                                       CEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEA
                                                                                                                                                                                                                                                                                                                           SWNH-----
SKFSSRMATHSSSVVSQDFSSEDSNDVFGSDAFAAFPEPMEPQMFSNLDLSEESDESPSM
                                      VQRKREMILKHKEEEALKESIKPK-LSEEQQKVIDTLLEAHHKTFDTTYSDFNKFRPPVR
                                                                                                                                     VEERRALIKKKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP--
                                                                                                                                                                                                                                                                              SWDEQQQSMAYLPDADMDTVAASTSLP-DPAGDFDRNV--PRICGVCGDRATGFHFNAMT
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47'
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451
15
112
67
107
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C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                       Score 815;
Pred. No. 5.
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VITAMIN D3
FOR FORM B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HINGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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VDR_XENLA
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                                                                              INTERPRO; IPRO00324;
INTERPRO; IPRO00536;
INTERPRO; IPRO00536;
INTERPRO; IPRO101628;
PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR000350; VITAMINDR.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDR_XENIA STANDARD: PRI; 422 AA.
013124;
013124;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97307679; PubMed-9165021;
L1 Y.C., Bergwitz C., Jueppner H., Demay M.B.
"Cloning and characterization of the vitamin
                                                                                                                                                                                                               EMBL; U91846; AAB58585.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrinology 138:2347-2353(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                               Receptor; Tr
Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laevia.
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DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.

TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED.
LEVEL IN SMALL INTESTINE AND SKIN.
DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASE
GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                               NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE EXPRESSION OF HORMONE SENSITIVE GENES.
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                                                                Transcription
 25
61
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85
                                                             regulation; DNA-binding; Nuclear protein;
C4-TYPE ZINC FINGERS (TWO)
C4-TYPE.
C4-TYPE.
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Best Local
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                              MEDLINE-89071726; PubMed-2849110;
Burmester J.K., Wiese R.J., Maeda N., Deluca H.;
"Structure and regulation of the rat 1,25-dihydroxyvitamin
                                                                                                                                                                                                                                                                                                                                                            VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR). VDR OR NR1I1.
                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                         Proc.
                                                                                                                                      CDNA. "
                                                                                                                                                Burmester J.K.; Maeda N., Deluca H.F.; "Isolation and expression of rat 1,25-dihydroxyvitamin
                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                   P13053;
01-JAN-1990
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                                                                                                                                                                                          SEQUENCE OF 58-423 FROM N.A.
                                                                                                                                                                                                                                     receptor.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                               MEDLINE-88124963; PubMed-2829212;
Burmester J.K.; Maeda N., Deluca
                                                                                                                                                                                                                                                                                                                                                                                                                                              VDR_RAT
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                                     C. Natl. Acad. Sci. U.S.A. 85:1005-1009(1988).
FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLL
THE EXPRESSION OF FORMONE SENSITIVE GENES.
SUBCELLULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR.
BODMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL
A DUA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAI
A DUA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAI
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                           NR1 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFA---TPLMQELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITL 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGR--LSYCLED-TAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPSEDSDVFTSSPDSSEHGFFSASLFGQFEYSSMGGKSGELSMLPHIADLVSYSIQKIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLKRCVDIGMMKEFILTDEEVQRKRQMINKRKSEEALKESMRPK-ISDEQQKMIDILLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICGYCGDKATGEHENAMTCEGCKGFFRRSMKRKAMFTCPF-NGDCRITKDNRRHCQSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHNMELLEPLYKFQVGLKKLDLHEEEHVLLMAICILSPDRPGLQDKALVESIQDRLSSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAKMIPGFRDLIAEDQIALLKSSVIEVIMLRSNQSFSLDDMSWTCGSEDFKYKVDDVTQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172;
                                                                                                                                                                                                                       Natl. Acad.
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                                                                                                                                                                                                                                                                                                                    Eutheria;
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189
422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ
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422 LI
48188 MW;
                                                                                                                                                                                                                                                                                                                   Chordata; (Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%;
41.1%;
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C8A9F25414FEE9D5 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              423
                                                                                                                                                                                                                                                                                                                                                                                       update)
                                        HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 422;
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                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
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                                                                                                                                                  D3
                                                                                                           CONTROLLING
                                                                                                                                                  receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                                                                                                                                 D3
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Best Local S
Matches 172
                               P48281;
01-FEB-1996 (Rel. 33, C
01-FEB-1996 (Rel. 33, I
15-JUL-1999 (Rel. 38, I
VITAMIN D3 RECEPTOR (VI
VDR OR NR1I1
                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PROSITE; PS00031; NUCLEAR RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T00882; -.
INTERPRO; IPR000324; -.
INTERPRO; IPR000536; -.
INTERPRO; IPR001628; -.
             Mus musculus
                                                                                                                                                                                    VDR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               363
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A31367; A31367.
P03372; 1HCQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 136
                                                                                                                                                                                                                                                                                                          PGSHQLYAKMIQKLADLRSLNEEHSKQYRSLSFQPENSMKLTPLVLEVFG
                                                                                                                                                                                                                                                                                                                                         PAHRELELKIMAMLTELRSINAQHTQ--RLLRIQDIHPE-ATPLMQELEG
                                                                                                                                                                                                                                                                                                                                                                                                                  IKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAKLVEAIQDRLSNTLQTYIRCRHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDVTDVSKAGHTLELIEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT---AGGFQQLLLEPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSGFSNLDLNGEDSD-----DPSVTLDLSPLSMLPHLADLVSYSIQKVIGFAKMIPGFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHKTYDPTYADFRDFRPPVRMDGSTGSYSPR----PTLSFSGNSSSSSSDLYTTSLDMME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAPSREEAAKWSQVRKDLCSLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQQHIIAILLDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICGYCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
          (Mouse)
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                                                                                                                                                                                       STANDARD;
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84
187
                                                            (VDR) (1,25-DIHYDROXYVITAMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47813 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 801; DB 1
42.0%; Pred. No. 7e-57;
                                                                                 Last sequence update;
Last annotation updat
                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE.
C4-TYPE.
HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C4-TYPE ZINC
                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1A0E519A9DCCE990 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 423;
                                                            D3
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INTERPRO; IPRO00536; -.
INTERPRO; IPRO01628; -.
INTERPRO; IPRO01628; -.
PRAM; PF00104; hormone_rec; 1.
PPAM; PF00105; zf-c4; 1.
PPAM; PF00047; STROIDFINGER.
PRINTS; PRO0047; STROIDFINGER.
PRINTS; PRO0031; NUCLEAR_RECEPTOR; 1
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor.";
Gene 152:281-282(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-95137405; PubMed-7835717;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamei Y., Kawada T.,
"Cloning and sequenc
                                                         243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:103076; VDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D31969; BAA06737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                               357
                                                                                                                       199
                                                                                                                                                                                 139
                                                                                                                                                                                                              197
                                                                                                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inc-finger;
                                                                                                                                                   240
                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN THE EXPRESSION OF HORMONE SENSITIVE GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE EXPRESSION OF HORMONE SENS SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NR1 SUBFAMILY.
ELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAKLVEAIQDRLSNTLQTYI
                                                                                                                                                                                                                                          RLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQQHIIAILLDA 138
                                                                                                                                                                                                                                                                       RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 196
                                                                                                                                                                                                                                                                                                                                  PQICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC
                             LLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYI
                                                         IPGFRDLTSDIQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDITDVSRAGHTL
                                                                              ISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT---AGGFQQ
                                                                                                                   TM--DL-----NEEGS----DDPSVTLDLSPLSMLPHLADLVSYSIQKVIGFAKM
                                                                                                                                                 QVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKV 299
                                                                                                                                                                                 HHKTYDPTYADFRDFRPPIRADVSTGSYSPRPTLSFSGDSSSNSDLYTPSLDMMEPASFS
                                                                                                                                                                                                             QMKTFDTTFSHFKNFRLP--GVLSSGCELP------ESLQAPSRE--EAAKWS
                                                                                                                                                                                                                                                                                                    PRICGYCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          422 AA;
                                                                                                                                                                                                                                                                                                                                                              Conservative
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                          47851 MW;
                                                                                                                                                                                                                                                                                                                                                          74;
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C4-TYPE.
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Pred. No. 3.4e-56;
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LIGAND-BINDING.
; 4704CC8172445732 CRC64;
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mouse vitamin D
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Matches 174
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SEQUENCE
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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"Nucleotide sequence of the bovine vitamin D3 receptor.";
J. Dairy Sci. 79:1313-1315(1996).
-I- EUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
                                                                                                                                                                                                                                                                                                         PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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15-JUL-1999 (Rel. 38, Last
VITAMIN D3 RECEPTOR (VDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDR_BOVIN
Q28037;
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SUBCELLULAR LOCATION: NUCLEAR.
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DO
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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                                                                       PQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECNRPQPAHRELELKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELEG
RLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEEALKDSLRPK-LSEEQQRIIAILLDA 135
                           RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 196
                                                    PRICGYCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC 76
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P03372;
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                                                                                                                           Similarity
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(Rel. 35, Last sequence update)
(Rel. 38, Last annotation update)
PROCEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                                                                                                                                                                           ; Phosphorylation.
21 86 C
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                                                                                                              Conservative
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1HCQ.
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Pred.
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E9E24926CE38CB7D
                                                                                                                                                                                                          C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
HINGE.
                                                                                                              Mismatches
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6.

    DNA-binding; Nuclear protein;

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.5e-56;
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                                                                                                                                       Length 424;
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Homo sapiens (Human).
Eukaryota: Metazoa; Chordata;
Eukaryota: Mutheria; Primates;
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P11473;
01-OCT-1989
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
01-OCT-2000 (Rel. 40, Last annotation
VTTAMTN D3 RECEPTOR (VDR) (1,25-DIHYD)
                                           sequencing.";
J. Biol. Chem.
                                                                                                                                                                            gene
VARIANTS ASP-33 AN MEDLINE-89072761;
                                                             SEQUENCE OF 24-90 FROM N.A.
TISSUE-PERIPHERAL BLOOD;
MEDLINE-91210272; PubMed-1850412;
Yu X.-P., McCharla H., Hustmyer F.G., Manolagas S.C.;
Yu Kanin D receptor expression in human lymphocytes.;
requirements and characterization by western blots and sequencing.";
                                                                                                                                                                                   MIYAMOTO K., Kesterson R.A., Yanamoto H., Ta
Tatsumi S., Inoue Y., Morita K., Takeda E.,
"Structural organization of the human vitami
gene and its promoter.":
                                                                                                                                                                                                                                                                                          TISSUE-LENS EPITHELIUM;
Rae J.L., Shepard A.R.;
Submitted (SEP-1997) to
                                                                                                                                                                                                                                                                                                                                                                 Goto H., Chen K.S., Prahl J.M., Deluca H.F.;

A single receptor identical with that from intestine/T47D mediates the action of 1,25-dhlydroxyvitamin D-3 in HL-60 c piochim. Biophys: Acta 1132:103-108(1992).
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MEDLINE-92379083; PubMed-1324736;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88217887; PubMed-2835767;
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                                           266:7588-7595(1991).
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WEDLINE-97120600; PubMed-8951271; WHITTINE-97120600; PubMed-8951271; Whitfield G.K., Selznick S.H., Haussler C.A., Hsieh J.-C., Galligan M.A., Jurutka P.W., Thompson P.D., Lee S.M., Zerwekh J.E., Haussler M.R.; "Vitamin D receptors from patients with resistance to 1,25-"Vitamin D(3): point mutations confer reduced transactivation in response to ligand and impaired interaction with the retinoid X receptor heterodimeric partner."; Mol. Endocrinol. 10:1617-1631(1996).
                                                                                                                                                                                                                                          vitamin D receptor
rickets.";
                                                                                                                                                                                                                                                                                                                                                                                                  basis of steroid structures.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malloy P.J., Weisman Y., Feldman D.;
"Hereditary 1 alpha,25-dihydroxyvitamin D-resistant rickets
from a mutation in the vitamin D receptor deoxyribonucleic
acid-binding domain.";
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"A unique mutation in the vitamin D receptor gene in three patients with vitamin D-dependent rickets type II: utility strand conformation polymorphism analysis for heterozygous detection.";
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"Point mutations in the human hypocalcemic rickets.";
Science 242:1702-1705(1988).
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"Two mutations in the hormone binding or 
receptor cause tissue resistance to 1, 
J. Clin. Invest. 92:12-16(1993).
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"A new point mutation in the deoxyribonucletc acid-binding
the vitamin D receptor in a kindred with hereditary
1,25-dihydroxyritamin D-resistant rickets.";
J. Clin. Endocrinol. Metab. 76:509-512(1993).
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                                                                                                                                                                                                                                                                                  Lin U.-T., Malloy "A novel mutation
                                                                                                                                                                                                                                                                                                                       MEDLINE-96272879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94149129; PubMed=8106618;
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                                                                                                                                                                                                                                                                                                                                              VARIANT ASP-46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95129267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93315633; PubMed=8392085;
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T., Marx S.J., Liberman U.A., Pike J.W.;
T., Marx S.J., Liberman U.A., Pike J.W.;
nique point mutation in the human vitamin D receptor chromosomonfers hereditary resistance to 1,25-dihydroxyvitamin D3.";
Endocrinol. 4:623-631(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                            mutations causing vitamin D
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                                                                                                                                                                                                                        Endocrinol. Metab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrinol. Metab. 78:313-316(1994).
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                                                                                                                                                                                                                                                           P.J., Sakati N., Al-Ashwal A., Feldman D.; in the deoxyribonucleic acid-binding domain of the causes hereditary 1,25-dihydroxyvitamin D-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                         hormone
                                                                                                                                                                                                                                                                                                                           PubMed-8675579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49:668-673(1991).
                                                                                                                                                                                  CYS-391
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                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor gene in three Japanese ickets type II: utility of single-alvsis for heterozygous carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , O'Riordan J.L.H., Hug
domain of the vitamin
,25 dihydroxyvitamin D:
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ling domain
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      INTERPRO; IPRO00324; ...
INTERPRO; IPRO00326; ...
INTERPRO; IPRO01628; ...
INTERPRO; IPRO01628; ...
PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4;i1.
PFAMS; PF00047; STROTDFINGER.
PRINTS; PR00047; STROTDFINGER.
PRINTS; PR00031; NUCLEAR_RECEPTOR; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
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MEDLINE-97158630; PubMed-9005998;
Malloy P.J., Eccleshall T.R., Gross C., van Maldergem L., leading D.;
Feldman D.;
"Hereditary vitamin D resistant rickets caused by a novel "Hereditary vitamin D resistant results in decreased affinity
                                                                                                                                                                                                                                          DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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EMBL;
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J. Clin. Invest. 99:297-304(1997)
                                                              VARIANT
                                                                                                   VARIANT
                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 601769; -. MIM; 277440; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [15]
VARIANT GLN-305.
                                                                                                                                                                                                                                                                                                       Zinc-finger;
                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                          DOMAIN
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- FUNCTION: VDR MEDLATES THE ACTION OF VITAMIN D3
THE EXPRESSION OF HORMORE SENSITIVE GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L; AF026260; AAB95155.1; -...
L; AB002168; BAA83389.1; JOINED.
L; AB002161; BAA83389.1; JOINED.
L; AB002163; BAA83389.1; JOINED.
L; AB002163; BAA83389.1; JOINED.
L; AB002165; BAA83389.1; JOINED.
L; AB002165; BAA83389.1; JOINED.
L; AB002167; BAA83389.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN A DNA-BLINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. DISEASE: DEFECTS IN UDR ARE THE CAUSE OF TYPE IIA RICKETS (ALSO KNOWN AS HYPOCALCEMIC VITAMIN D-RESISTANT RICKETS (HYDRR)). HYDRR IS MOST FREQUENTLY AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY SEVERE RICKETS, HYPOCALCEMIA AND SECONDARY HYPERPARATHYROLDISM SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: IT IS UNCERTAIN, WHETHER MET-1 OR MET-4 IS THE INITIATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NR.1
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X67482; CAA47824.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY
                                                                                                                                                                            Transcription regulation; DNA-binding; Nuclear protein; Phosphorylation; Disease mutation.

24 89 C4-TYPE ZINC FINGERS (TWO).

24 44 C4-TYPE
60 84 C4-TYPE.
90 191 HINGE.
192 427 LIGAND-BINDING.
33 3 G-> D (IN RICKETS).
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                      /FTId=VAR_004658.
G -> D (IN RICKETS).
/FTId=VAR_004659.
F -> I (IN RICKETS).
                                                                                                                                         LIGAND-BINDING.
G -> D (IN RICKETS).
/FTIG-VAR_004656.
H -> Q (IN RICKETS).
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K -> E (IN RICKETS).
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Best Local
                                                                                                                                                                                    MEDILINE-9415827; pubmed-8114692;

Baes M., Gullck T., Choi H.S., Martinoli M.G., Simha D., Moore D.D.

Baes M., Gullck T., Choi H.S., Martinoli M.G., Simha D., Moore D.D.

"A new orphan member of the nuclear hormone receptor superfamily the subset of retinoic acid response elements.";

Mol. Cell. Biol. 14:1544-1552(1994).

-I- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RECEPTOR ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES.

-I- SUBGULIULAR LOCATION: NUCLEAR (BY SIMILARITY).

-I- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER.

-I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ORPHAN NUCLEAR RECEPTOR NRII3 (CONSTITUTIVE ANDROSTANE RECEPTOR) (CAR)
(ORPHAN NUCLEAR RECEPTOR MB67).
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Q14994;
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                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMEL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHKTYDPTYSDFCQFRPPVRVNDGGGSHPSRPNSRHTPS--FSGDSSSSCSDHCITSSDM
                                                                                                                                                                        SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%;
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Pred. No. 6.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R -> Q (IN RICKETS).
/FTId-VAR_004661.
R -> Q (IN RICKETS).
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and for commercial
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Best Local Similarity
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ZN_FING
ZN_FING
SEQUENCE
                                                                                                                             NRI3_RAT STANDARD; PRT; 358 AA.
09QUS1;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0RPHAN NUCLEAR RECEPTOR NRII3 (CONSTITUTIVE ANDROSTANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00105; zf-C4; 1.
PRINTS; PR00047; STROLDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00546; THXROIDHORNE.
PROSITE; PR00031; NUCLEAR_RECEPTOR; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; 21nc-finger; Activator.
DNA_BIND 11 76 C4-TYPE ZINC FINGERS (TWO).
ZN_FING 11 31 C4-TYPE.
ZN_FING 47 71 C4-TYPE.
SEQUENCE FROM N.A.
STRAIN-WISTAR KYOTO, AI
YOShinari K., Sueyoshi
                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                        RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPROC0324; -.
INTERPRO; IPROC0536; -.
INTERPRO; IPROC1628; -.
INTERPRO; IPRO01728; -.
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                                                                                                     NR1I3 OR CAR.
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                                                                                                                                                                                                                                                                             LRSINEAYGYQIQHIQGLSAM-MPLLQEI
                                                                                                                                                                                                                                                                                                          LRSINAQHTQRLLRIQDIHPFATPLMQEL 467
                                                                                                                                                                                                                                                                                                                                     YVLLAAMALFSPDRPGVTQRDEIDQLQEEMALTLQSYIKGQQRRPRDRFLYAKLLGLLAE
                                                                                                                                                                                                                                                                                                                                                             YVLMQAISLESPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMGTMFEQFVQFRPPAHLFIHHQ-PLPTLAP----------------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 AA;
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AND FISCHER; TISSUE-LIVER; hi T., Moore R., Negishi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 768; DB 1;
Pred. No. 2.4e-54;
2; Mismatches 109
                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92EAAD07D7DCB9DA CRC64
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Best Local (
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INTERPRO; IPRO01723; -.
INTERPRO; IPRO01728; -.
INTERPRO; IPRO01728; -.
PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PFAM; PF00105; zf-C4; 1.
PFAMTS; PR00347; STROIDFINGER.
PRINTS; PR00359; VITAMIUNR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZN_FING
ZN_FING
SEQUENCE
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RECEPTOR ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES (BY SIMILARITY).
-!- SUBUNIT: HETERODIMER OF NRII3 AND RXR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO;
INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF133095; AAF22567.1; -. EMBL; AF133094; AAF22566.1; -. INTERPRO; IPR000324; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger; Activator.
DNA_BIND 21 86
ZN_FING 21 41
ZN_FING 57 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
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                                                                                                                                                                           KLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFL 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRR 131
KLMGLLAELRSINSAYSYEIHRIQGLSAM-MPLLGEI
                                  KIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQEL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLLGAHTRHVGPMFDQFVQFRPPAYLFSH-HRPFQPLAP---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEEYGPRNCVVCGDRATGYHFHALTCEGCKGFFRRTVSKTIGPICPF-AGRCEVSKAQRR 71
                                                                                                                      RLQLQEPEYALMAAMALFSPDRPGVTQREEIDQLQEEVALILNNHIMEQQSRLQSRFLYA
                                                                                                                                                                                                                                      ISLLKGAAVEILHISLNTTFCLQTQNFFCGPLCYKMEDAVHVGFQYEFLELIIHFHKTLK
                                                                                                                                                                                                                                                                                                 ISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAG-GFQQLLLEPMLKFHYMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000536; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.28;
                                                                                                                                                                                                                                                                                                                                                         ----VLPLLTHFADINTEMVQQIIKFTKDLPLFRSLTMEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 729; DB 1; I
Pred. No. 3.3e-51;
1; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C4-TYPE ZINC FINGERS (TWO)
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13691F49CAD8F1ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                 370
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RESULT 13

NRI3_MOUSE STANDARD; PRT; 358 AA.

ID NRI3_MOUSE STANDARD; PRT; 358 AA.

AC 035627; 035628;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE 0RPHAN NUCLEAR RECEPTOR NRII3 (CONSTITUTIVE ANDROSTANE RECEPTOR)
  EMBL; AF009327; AAC53349.1; -.
EMBL; AF009328; AAC53350.1; -.
MGD; MGI:1346307; NR113.

INTERPRO; IPR000324; -.
INTERPRO; IPR000324; -.
INTERPRO; IPR001628; -.
INTERPRO; IPR001723; -.
INTERPRO; 
DNA_BIND
ZN_FING
ZN_FING
VARSPLIC
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00031; NUCLEAR_RECEPTOR: 1.

Receptor: Transcription regulation; DNA-binding; Nuclear Zinc-finger; Activator; Alternative splicing.

DNA_BIND 21 86 C4-TYPE ZINC FINGERS (TWO).

ZN_FING 21 41 C4-TYPE.

ZN_FING 21 41 C4-TYPE.

ZN_FING 21 41 C4-TYPE.

ZN_FING 21 41 C4-TYPE.

VARSPLIC 281 286 DREGVT -> GFCMQS (IN ISOFORM CAR2).

VARSPLIC 287 358 MISSING (IN ISOFORM CAR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NR1I3 OR CAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Differential transactivation by two isoforms of the orphan nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moore D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi H.-S., Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97442417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A TRANSACTIVATOR.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NR1 SUBFAMILY.
281
287
358 NA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9295294;
M., Tzameli I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
     40894
     MW;
DRPGVT -> GFCMQS (IN ISOFORM CAR2).
MISSING (IN ISOFORM CAR2).
; 4F07730FF78CADBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simha D., Lee Y.-K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
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                                                           HSSP;
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRH2_HUMAN STANDARD; PRT; 461 AA.
P55055;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OXYSTEROLS RECEPTOR LXR-BETA (LIVER X RECEPTOR BETA) (NUCLEAR ORPHAN RECEPTOR LXR-BETA) (UBIQUITOUSLY-EXPRESSED NUCLEAR RECEPTOR) (NUCLEAF
                                                                                                                                                                                                                                                                                                                                                                     Gene
                                                                                                                                                                                                                                                                                                                                                                             TISSUE-OSTEOSARCOMA;
MEDLINE-95011628; PubMed-7926814;
Shinar D.M., Endo N., Rutledge S.J., Vogel R.,
"NER, a new member of the gene family encoding
hormone nuclear receptor.";
                           INTERPRO;
                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NR1H2 OR LXRB OR UNR OR NER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
           NTERPRO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
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FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO I COLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS SEQUENCE 5'- AGGTCA-3' AND 4-NT SPACING (DR-4).

SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                             600380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAKLMGLLADLRSINNAYSYELQRLEELSAM-TPLLGEI 356
                                                         U07132;
P03372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQEL 467 : |:|:|:|:|:|:|:|:|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQISLLKGAAVEILHISLNTTFCLQTENFFCGPLCYKMEDAVHAGFQYEFLESILHFHKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQISLLKGAAFELCQLRENTVFNAETGTWECGRLSYCLEDTA-GGFQQLLLEPMLKFHYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKGLHLQEPEYVLMAATALFSPDRPGVTQREEIDQLQEEMALILNNHIMEQQSRLQSRFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRHCPACRIQKCINVGMRKDMILSAEALALRRARQAQRRAEKASIQ------LNQQQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRQCQACRIRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *-----FMHHRPEQPRG--PVLPLLTHEADINTEMVQQIIKFTKDLPLFRSLTME
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                                                                                                                                                                                                                                        SUBFAMILY.
           IPR000536; -. IPR001628; -.
                                                           1HCQ.
                                                                        AAA61783.1;
                                                                                                                                                                                                                                                                                                                                                                                              Rodan G.A.
the human
                                                                                                                                                                                                                                                                                                                                                                                                               G.A.,
                                                                                                                                                                                                                                                                                                                                DOUBLE-STRANDED
HALF-SITE
                                                                                                                                                                                                                                                                                                                                                                                                steroid
                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt
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Best Local
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                                                                                                                                                                                                                                                          _MOUSE
NRH3_MOUSE
                                                                                                         ABCLE.
NRIH3 OR LXKA.
NRIH3 OR LXKA.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazia; Rodentia;
                                                                                                                                                                               092019;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
0XYSTEROLS RECEPTOR LXR-ALPHA (LIVER X RECEPTOR ALPHA) (NUCLEAR ORPHAN
Chen Y.E., HOTIUCHI M., DZAU V.J.;
SUDMITTEG (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH
SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER
ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPO
THROUGH TARGET GENES DEFINED BY LXRES (BY SIMILARITY).
-!- SUBCELLULAR, LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                               RECEPTOR LXR-ALPHA).
NR1H3 OR LXRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
ZN_FING
ZN_FING
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 PRGPEANLE-VRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCGDKATGYH
                                                                                                                                                                                                                                                                                                                       SYTRIKRPQDQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPPLLSEIWDV
                                                                                                                                                                                                                                                                                                                                                    SYIECNRPOPAHRFLFLKIMAMLTELRSINAOHTORL--LRIQDIHPFATPLMQELFGI
                                                                                                                                                                                                                                                                                                                                                                                                  FQQLLLEPMLKFHYMLKKLQLHEEEYYLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLK
                                                                                                                                                                                                                                                                                                                                                                                                                                    QVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET - - - ECITFLKDFTYSKDDFHRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWEC----GRLSYCLED-TAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNVMTCEGCKGFFRRAMKRNARLRCFFR-KGACEITRKTRRQCQACRLRKCLESGMKKEM 150
                                                                                                                                                                                                                                                                                                                                                                               LQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPGRVEALQQPYVEALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVQLTAAQELMIQQLVAAQLQCNKRSFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMSDEAVEERRALIKRKKSERTGTQ---PLGVQG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNVLSCEGCKGFFRRSVVRGGARRYACRGGGTCQMDAFMRRKCQQCRLRKCKEAGMREQC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLSEEQIRKKK;-IRKQQQQESQSQSQSPVGPQGSSSSASGPGASPGGSEAGSQGSGEGE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGGPDPDVPGTDEASSACSTDWVIPDPEEEPERKRKKGPAPKMLGHELCRVCGDKASGFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
87
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173
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Pred. No. 9.
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POLY-GLN.
POLY-SER.
                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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C4-TYPE.
C4-TYPE.
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                        RESPONSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF085745; AAD16050.1; -. HSSP; P20393; 1A6Y. INTERPRO; IPR000536; -. INTERPRO; IPR001628; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRODUCT; STROIDFINGER.

PROSITE; PSO0031; NUCLEAR_RECEPTOR; 1.

Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00104; hormone_rec; 1. PFAM; PF00105; zf-C4; 1.

    -i- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
    NR1 SUBFAMILY.

                                                                                                                                                                                                                                                                                                                                 171 ---RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESL 227
| : | : | | | | : | : | | : | 228
190 VSPRVSSPPQVLPQLSPEQLGMIEKLVAAQQQCNRRSFS------ 228
                                                                                                                                                                                                                                                                                                                                                                                                   117 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 170
                                                                                                                                                                                             436 LLSEIWDV 443
                                                               380 QHTYVEALHAYVSINHPHDP--LMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP 435
                                                                                            405 QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 462
                                                                                                                                320 NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPŇVQDQLQVERL 379
                                                                                                                                                             346 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQL 404
                                                                                                                                                                                                                                                                463 LMQELFGI 470
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                                                                                                                                                                                                                                                                                                 QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 AA;
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116
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50417 MW;
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C4-TYPE.
C4-TYPE.
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Search completed: February 18, 2001, 13:43:39 Job time: 5859 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: February 18, 2001, 14:33:07; Search time 57.29 Seconds (without alignments) 560.604 Million cell updates/sec

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

US-09-143-828-4
2494
1 MTVTRTHHFKEGSLRAPAIP......QDIHPFATPLMQELFGITGS 473

Scoring table:

195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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A45700	10100	T51096	A41055	A56558	A57035	D36067	A40377	A31820	TVHUAR	C36067	I51165	S58211	TVCHTB	149018	A56918	I59354	149021	138975	A56043	JC4014	A56197	S24174	A28200	JC7230	PC4019	A31761	I50451	JC7229	S41497		ID
10011010 0010 1000	9 10 10 10	~	ecdysone receptor	retinoic acid rece	thyroid hormone be		hormone	thyroid hormone re	hormone	thyroid hormone re	gene c-erbA-beta p	beta-thyroid hormo	thyroid hormone re	retinoid X recepto	farnesoid x-activa	orphan nuclear rec	retinoid X recepto	nuclear orphan rec	steroid hormone re		nuclear hormone re	vitamin D'receptor	vitamin D receptor	vitamin D receptor	vitamin D receptor	1,25-dihydroxyvita	D U	vitamin D receptor	thyroid hormone re		Description

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probable transcrip	C40045	955 4		422	٠.
retinoic acid rece	B56558		۰	422	-
nuclear receptor I	S52913		0	423	۳
retinoic acid rece	S06123	458 2	0	423	~
retinoic acid rece	S78481		0	424	_
thyroid hormone re	A32608		ö	424.5	_
ecdysteroid recept	A56590			424.5	•
retinoic acid rece	S13512			425	۳
thyroid hormone re	TVCHVR	408 1		425.5	•
retinoic acid rece	805051	148 2	'n	427	٠.
nuclear receptor R	A57048		Ļ	427.5	٠.
nuclear receptor F	JC2494		່ພ	428	_
retinoic acid rece	A41977		'n	428	_
retinoic acid rece	S02827	148 2	'n	428	
orphan nuclear hor	A57057		'n	429	
retinoic acid rece	I51256		w	432	_

ALIGNMENTS

	QY 415 YIECNR-POPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFG 469	
	OY 355 QOLLLEDMIKFHYMIKKIQIHEEEYVIMQAISLESPDRPGVIQHRVVDQIQEQFAITIKS 414	
	OY 296 FAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT-AGGF 354 :: : : : : : : : :: ::	
	OY 236 AKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIIS 295	
	Qy 176 PLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEA 235	
	QY 117 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRK-KSERTGTQ 175 : :	
	Qy 57 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 116	
9	Query Match 39.8%; Score 991.5; DB 2; Length 386; Best Local Similarity 49.0%; Pred. No. 8.4e-70; Matches 204; Conservative 59; Mismatches 104; Indels 49; Gaps	
homology	.53006.1; piD:g410518 transforming protein ;RBA>	
Lates with	R;Smith, D.P.; Mason, C.S.; Jones, E.A.; Old, R.W. Nucleic Acids Res. 22, 66-71, 1994 A;Title: A novel nuclear receptor superfamily member in Xenopus that associates A;Reference number: S41497; MUID:94173664 A;Accession: S41497 A;Status: prelighinary: nucleic acid sequence not shown	
	RESULT 1 S41497 thyroid hormone receptor homolog - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 20-May-1994 *sequence_revision 26-May-1995 *text_change 20-Sep-1999 C;Accession: S41497; S38486	

10;

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C; Keywords:
                                                                                                                                                                      vitamin D receptor isoform A - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
C:Accession: I50451
R:Elaroussi, M.A.; Prahl, J.M.; Deluca, H.F.
Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994
A:Title: The avian vitamin D receptors; primary structures; and their origins.
A:Reference number: I50451; MUID:95062315
A:Accession: I50451
A;Cross-references: EMBL:U12641; NID:g595500; PIDN:AAA56725.1; PID:g595501
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein
C;Keywords: zinc finger
                                                                                        A; Molecule type: mRNA
A; Residues: 1-448 <ELA>
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C;Keywords: bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: DDBJ:AB037673
A;Experimental source: intestine
C;Comment: This receptor is an important factor in calcium homeostasis and bone formati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 09-Jun-2000 #Sequence_revision 09-Jun-2000 #text_change 18-Aug-2000 C;Accession: JC7229
C;Accession: JC7229
R;Suzuki T: Suzuki, N.; Srivastava, A.S.; Kurokawa, T.
Biochem. Biophys. Res. Commun. 270, 40-45, 2000
A;Title: Identification of cDNAs encoding two subtypes of vitamin D receptor A;Reference number: JC7229
A;Accession: JC7229
                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-420 <SUZ>
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C;Species: Paralichthys olivaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: unassigned erbA-related proteins; erbA transforming protein homology; Reywords: bone; calcium transport; DNA binding; hormone receptor; intestine; vita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 CNRPQPAHRFLELKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 PGFRDLTAEDQIALLKSSAIEIIMLRSNQSFSLEDMSWSCGGPDFKYCINDVTKAGHTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 RMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSSGCELPESLQAPSREEAAKWSQVRK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 RKTRRQCQACKLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 VNADE-EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEIT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARMISSLVEAHHKTYDASYSDFSRFRPPVREGPVTRSASRAASLHSLSDASSDSFNHSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN--HPGGRLLYAKMIQKLADLRSLNEEHSKQYRSLSFQPEHSMQLTPLVLEVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLEPLVKFQVGLKKLNLHEEEHVLLMGICLLSPDRPGVQDHARVEQLQDRLPEALQAYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECG--RLSYCLED-TAGGFQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SV-DTKMNFSNLLMMYQDGA----SSPDSSEENTKLSMLPHLADLVSYSIQKVIGFAKMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGPDEFDRNAPRICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKASFTCPF-NGSCTIT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDNRRHCQACRLKRCIDIGMMKEFILTDEEVQREKEMILKRKEEEAAREAMRPR-LNEEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.8%; Score 817; DB 2; 43.1%; Pred. No. 3.8e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469
                               protein homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intestine; vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
    367
                                              395
                                                                                      307
                                                                                                                              338
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                                                                                                                                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                    172 TGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP-------GVL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSER 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 CESQELQSSDMETPAVGTPEFDRNVPRICGVCGDRATGFHFNAMTCEGCKGFFRRSMKRK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 CEDTE---SYPGKPSVNADE-EVGGPQICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRN 111
VQDTSLVESIQDRLSDTLQTYIRCRHPPPGSRLLYAKMIQKLADLRSLNEEHSKQYRCLS 426
                                                                                                                                                                        MLPHLADLVSYSIQKVIGFAKMIPGFRDLTAEDQIALLKSSAIEVIMLRSNQSFTMEDMS
                                                                                                                                                                                                              LLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGT 337
                                                                                                                                                                                                                                                                                                                                                                                                                              AMFTCPF-SGDCKITKDNRRHCQACRLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEE 134
                                          VLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLR 452
                                                                                 WTCGSNDFKYKVSDVTQAGHSMDLLEPLVKFQVGLKKLNLHEEEHVLLMAICILSPDRPG
                                                                                                                            WECGR--LSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPG 394
                                                                                                                                                                                                                                                        SQDFSSEDSNDVFGSDAFGAFPEPMEPQMFSNLDLSEESDESPSMNIELPH-----LP
                                                                                                                                                                                                                                                                                               SSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFS 277
                                                                                                                                                                                                                                                                                                                                            ALKESLKPK-LSEEQQKVINILLEAHHKTFDTTYSDFNKFRPPVRSKFSSSTATHSSSVV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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40.9%; Pre-
72;
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Pred. No. 5.4e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 448;
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                                                                                    366
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A31761
1, 25-dihydroxyvitamin D-3 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Dete: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999
R;Burmester J.K; Wiese, R.J.; Maeda, N.; DeLuca, H.F.
A;Residues: 1-423 <BUR>
A;Coss-references: GB:J04147; GB:J03630; NID:g203956; PIDN:AAA41089.1; PID:g203957
R;Burmester J.K; Maeda, N.; DeLuca, H.F.
Proc. Natl. Acad. Sci. U.S.A. 85, 1005-1009, 1988
A;Title: Isolation and expression of rat 1,25-dihydroxyvitamin D-3 receptor cDNA.
A;Reference number; A31367; MUID:88124963
A;Reference number; A31367; MUID:88124963
A;Residues: 'R',58-423 <BUZ>
C;Superfamily: unassigned protein function; crim finger
F;22-337/Domain: erbA transforming protein homology
F;24-44/Region: zinc finger
F;20-84/Region: zinc finger
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C;Species: Mus musculus (house mouse)
C;Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
C;Accession: PC4019
R;Kamel, Y; Kawada, T; Fukuwatari, T; Ono, T; Kato, S; Sugimoto, E.
Gene 152, 281-282, 1995
A;Title: Cloning and sequencing of the gene encoding the mouse vitamin D receptor.
A;Reference number: PC4019
A;Accession: PC4019
A;Accession: PC4019
A;Ccoss-references: DDBJ:D31969; NID:g699618; PIDN:BAA06737.1; PID:d1007311; PID:g6996
A;Cross-references: DDBJ:D31969; NID:g699618; PIDN:BAA06737.1; PID:d1007311; PID:g6996
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: DNA binding; zinc finger
F;22-336/Domain: erbA transforming protein homology <F;24-89/Domain: DNA binding #status predicted <BIN>
F;191-422/Region: vitamin D binding #status predicted
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;Species: Mus musculus (house mouse)
;Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                       77 PQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCFFRKGACEITRKTRRQCQAC 136
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKFHYMLKKIQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQIQEQFAITLKSYIECNRPQ 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HHKTYDPTYADFRDFRPPVRMDGSTGSYSPR----PTLSFSGNSSSSSSDLYTTSLDMME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQQHIIAILLDA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGSHQLYAKMIQKLADLRSLNEEHSKQYRSLSFQPENSMKLTPLVLEVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAKLVEAIQDRLSNTLQTYIRCRHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDVTDVSKAGHTLELIEPL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPIEDQISLLKGAAFELCOLRENTVFNAETGTWECGRLSYCLEDT---AGGFQQLLLEPM 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSGFSNLDLNGEDSD-----DPSVTLDLSPLSMLPHLADLVSYSIQKVIGFAKMIPGFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRD 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAPSREEAAKWSQVRKDLCSLKV----
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                                                                                                                     QVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKV 299
                                                                                                                                                           HHKTYDPTYADFRDFRPPIRADVSTGSYSPRPTLSFSGDSSSNSDLYTPSLDMMEPASFS
                                                                                                                                                                                          QMKTFDTTFSHFKNFRLP--GVLSSGCELP------ESLQAPSRE--EAAKWS
                                                                                                                                                                                                                                                                    RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 196
                                                                                                                                                                                                                                                                                                        PRICGYCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC
                 IPGFRDLTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDITDVSRAGHTL
                                                 ISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT----AGGFQQ
                                                                                                                                                                                                                              RLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQQHIIAILLDA
                                                                                                                                                                                                                                                                                                                                                                                174;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                               31.8%;
                                                                                     NEEGS----DDPSVTLDLSPLSMLPHLADLVSYSIQKVIGFAKM
                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                               Score 792.5; DB 2; Pred. No. 3.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                127;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 422;
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C; Species: Homo sapiens (man)
C; Date: 19-May-1989 #sequence_revision
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                                vitamin D receptor - human
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Best Local
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vitamin D receptor subtype b - Paralichthys olivaceus
C;Species: Paralichthys olivaceus
C;Date: 09-Jun-2000 *sequence_revision 09-Jun-2000 *text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: vdr-b
C; Superfamily: unassigned
C; Keywords: bone; calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T.
Biochem. Biophys. Res. Commun. 270, 40-45, 2000
A;Title: Identification of cDNAs encoding two subtypes of vitamin D receptor in floun
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A;Experimental source: intestine
C;Comment: This receptor is an important factor in calcium homeostasis and bone forma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-425 <SUZ>
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A; Accession: JC7230
                                                        460 ATPLMQELFG; 469
                                                                                                                 354 ALQDRLSETLQAYIQLH--HPGGRLLYAKMIQKLADLRSLNEEHSKQYRSLSFRPEHSMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SVPGKPSVNADE-EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKK------SERT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCRHPPPGSHQLYAKMIQKLADLRSLNEEHSKQYRSLSFQPENSMKLTPLVLEVFG 418
                                                                                                                                                                    OLQEQFAITLKSYIECNRPOPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-
                                                                                                                                                                                                                                KYQISDVTKAGHTLELLEPLVKFQVGLKKLNLQEEEHVMLMAICLLSPDRPGVQDHARIE
                                                                                                                                                                                                                                                                       SYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVD
                                                                                                                                                                                                                                                                                                                                              VSYSIQKVIGFAKMIPGFRELTAEDQIALLKSSAIEVIMLRSNQSFNLEDMSWSCGAPDF
                                                                                                                                                                                                                                                                                                                                                                            STYMFKGIIŞFAKVISYFRDLPIEDQISLLKGAAFELCOLFENTVFNAETGTWECGR--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSDASSDSFSHSPESV-DTKVNFNNLLMMYQEQGS----SPDSSEEEGSSFSMLPHLADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARRP----RLTDEQSQVIAMLVEAHHKTYDDSYSDFCRFRPPVREGPVTRSASRAASLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSSGCELPESLQA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGSCTITKDNRRHCQACRLKRCVDIGMMREFILTDEEVQRKKDLIQRRKDEEAQREAERE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSREEAAKWSQVRKDLCSLKVS----LQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADM 285
LIPLVLEVSG 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erBA-related proteins; erbA transforming protein homology transport; DNA binding; intestine; vitamin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 790.5; DB 2;
; Pred. No. 4.5e-54;
78; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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19-May-1989 #text_change 20-Sep-1999

Accession: A28200; I55353

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C:Species: Rattus norvegicus (Norway rat)
C:Decies: Rattus norvegicus (Norway rat)
C:Decies: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 31-Oct-1997
C:Accession: S24174
R:Goto, H:; Chen, K:; Prahl, J.M.; DeLuca, H.F.
Biochim. Biophys. Acta 1132, 103-108, 1992
A:Title: A single receptor identical with that from intestine/T47D cells mediates the ac A:Reference number: S24174; MUID:92379083
                                                                                                                                                                                                                                                                          RESULT
S24174
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C;Superfamily: unassigned erbA-related proteins; erbA transforming C;Keywords: DNA binding; transcription regulation; zinc finger F;22-341/Domain: erbA transforming protein homology <ERBA>F;24-44/Region: zinc finger F;60-84/Region: zinc finger
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A;Title: Cloning and expression of full-length cDNA encoding human vitamin D receptor. A;Reference number: A28200; MUID:88217887

A;Accession: A28200

A;McDonnell type: mRNA
A;Residues: 1-427 <BAK>
A;Residues: 1-427 <BAK>
A;Cross-references: GB:J03258; NID:g340202; PIDN:AAA61273.1; PID:g340203
A;Cross-references: GB:J03258; NID:g340202; PIDN:AAA61273.1; PID:g340203
A;Yu, X.P.; Mocharla, H.; Hustmyer, F.G.; Manolagas, S.C.
J. Biol. Chem. 266, 7588-7595, 1991
A;Title: Vitamin D receptor expression in human lymphocytes. Signal requirements and characterior. F5353; MUID:91210272
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A;Gene: GDB:VDR
A;Cross-references: GDB:120487; OMIM:601769; OMIM:277440
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A;Molecule type: mRNA
A;Residues: 24-90 <RES>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          372 PPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLVLEVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 MDSSSFSNLDLSEEDSD-----DPSVTLELSQLSMLPHLADLVSYSIQKVIGFAKMIPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 HHKTYDPTYSDFCQFRPPVRVNDGGGSHPSRPNSRHTPS--FSGDSSSSCSDHCITSSDM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 PRICGYCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWTCGNQDYKYRVSDVTKAGHSLELIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSY----CLEDTAGGFQQLLLE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 789; DB 2; 42.2%; Pred. No. 5.9e-54;
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200 TFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDG

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-348 <BAES
A;Cross references: (.B:Z30425; GB:L29263; NID:g458541; PIDN:CAA83016.1; PID:g458542
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: zinc finger
E;9-270/Domain: erbA transforming protein homology <ERBA>
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A;Title: A new orphan member of the nuclear hormone receptor superfamily that A;Reference number: A56197; MUID:94158827
A;Accession: A56197
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A;Residues: 1-427 <GOTN
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: DNA binding; transcription regulation; zinc finger
F;22-341/Domain: erbA transforming protein homology <ERBA>
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Best Local :
                                                140 KCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 PLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRH 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 RLRKCLESGMXKEMIMSDEAVEERRALIKRKKSERTGTOPLGVQGLTEEQRMMIRELMDA 196
                                                                                                  11 CVVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPF-AGSCEVSKTQRRHCPACRLQ 69
                                                                                                                                                     80 CRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCFFRKGACEITRKTRRQCQACRLR 139
                                                                                                                                                                                                                                   Match 30.8%; Score 768; DB 2 Local Similarity 42.2%; Pred. No. 2e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 PQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQ-DIHPFATPLMQELFG
KCLDAGMRKDMILSAEALALRRAKQAQRRAQQTPVQ-----LSKEQEELIRTLLGAHTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLYLEVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMKTFDTTFSHFKNFRLPGVLSSG----CELPESLQAPSREEAAKWSQVRKDLC----- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSY---CLEDTAGGFQQLLLE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDLTSEDQIVILKSSAIEVIMLRSNESFTMDDMSWTCGNQDYKYRVSDVTKAGHSLELIE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174;
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                        62; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
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Pred. No. 5.9e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                           DB 2; Length 348;
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                                                                                                                                                                                                        Gaps
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Db 159 VLSEEQIRKKKIRKQQQESQSQSQSSQSGSGSAGSQGSGEGE 216 Qy 182LTEEQRMMIRELMDAQMKTEDTTESHFKNEFLDGVLSSGCELPESLQAPSREEAAKW 238	Query M Best Loc Matches 33 39 92 92	32; NID:g641 DBATCOMA Cel DBATCOMA:60 13.3 TECEPTOR FORMING PROTECTION FORMING PROTECTION	SULT Spec Spec Shin Shin Shin Shin Shin Shin Shin	
OF CHARLES LECKRE PARK FLEXINA AND CHARLES IN A CHICKLE I	190 VSPRVSSPPQVLPQLSPEQLGMIEKLVAAQQQCNRRSFS	Query Match Query Match Best Local Similarity 30.1%; Pred. No. 4e-31; Best Local Similarity 30.1%; Pred. No. 4e-31; Matches 129; Conservative; 84; Mismatches 144; Indels 71; Gaps 13; Qy 57 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 116	ll-Dec ion: A55 ion: A50 ion	87 G-0 9-8

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A;Cross-references: EMBL:U22662; NID:g726512; PIDN:AAA85856.1; PID:g726513
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: zinc finger
F;96-367/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway. A;Reference number: 138975; MUID:95262897
A;Accession: 138975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-447 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Endocrinol. 9, 72-85, 1995
A;Title: Isolation of proteins that interact specifically with the retinoid X receptor: A;Reference number: A57664; MUID:95280959
A;Accession: I49021
A. Reference in the control of proteins that interact specifically with the retinoid X receptor: A;Reference number: A57664; MUID:95280959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retinoid X receptor interacting protein No.15 - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999 C;Accession: 149021 C;Accession: 14902
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A;Cross-references: EMBL:U09419; NID:g691713; PIDN:AAC52164.1; PID:g691714 C;Genetics: A;Gene: RIP15 C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Reywords: zinc finger C;Reywords: z
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A;Molecule type: mRNA
A;Residues: 1-446 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 VSVQEIVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 287
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Pred. No. 9.8e-31;
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A;Molecule type: mRNA
A;Residues: 1-32,'V',34-51,55-218,'V',220-446 <RE2>
A;Cross-references: EMBH:U14533; NID:9565661; PIDN:AAA52361.1; PID:9565662
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                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL:UZ0389; NID:9665941; PIDN:AAA69522.1; PID:9665942
A; Experimental source: Sprague-Dawley, hepatic
R; Song, C.; Kokontis; J.M.; Hilpakka, R.A.; Liao, S.
Proc. Natl. Acad. Sci. U.S.A. 91, 10809-10813, 1994
A; Title: Ubiquitous receptor: a receptor that modulates gene activation by retinoic a A; Reference number: T59264; MUID:95062154
A; Accession: I59264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G;Accession: I59354; I59264
R;Teboul, M; Enmark, E; L1, Q; Wikstrom, A.C.; Pelto-Huikko, M.; Gustafsson, J.A.
Proc. Natl. Acad. Sci. U.S.A. 92, 2096-2100, 1995
A;Title: OR-1, a member of the nuclear receptor superfamily that interacts with the GA;Reference number: I59354; MUID:95199298
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                                                                                                                                           A; Experimental source: vagina C; Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C; Keywords: DNA binding; zinc finger ____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       orphan nuclear receptor OR-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I59354
                                                                                                                F;76-366/Domain: erbh transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                       A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 LCRLRKCKEAGMREQCVLSEEQIRKKR--IQKQQQQQPPPPSEPAASSSGRPAASPGTSE 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 APSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTY 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 YSKDDFHRAGIQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPSRVEA 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 IQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFAT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 GHELCRYCGDXASGFHYNYLSCEGCKGFFRRSYYHGGAGRYACRGSGTCQMDAFMRKCQ 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQ 403
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al Similarity
138; Conserv
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25; Conservative
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                          19.6%;
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                          Pred.
                             Score 488; DB 2;
Pred. No. 1.8e-30;
     Mismatches 174;
                                                           Length 446;
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13 SLRAPAIPLHSAAAELASNHPRGPEANLEVRP---KESWNHADFVHCEDTESVP-GKPSV 68

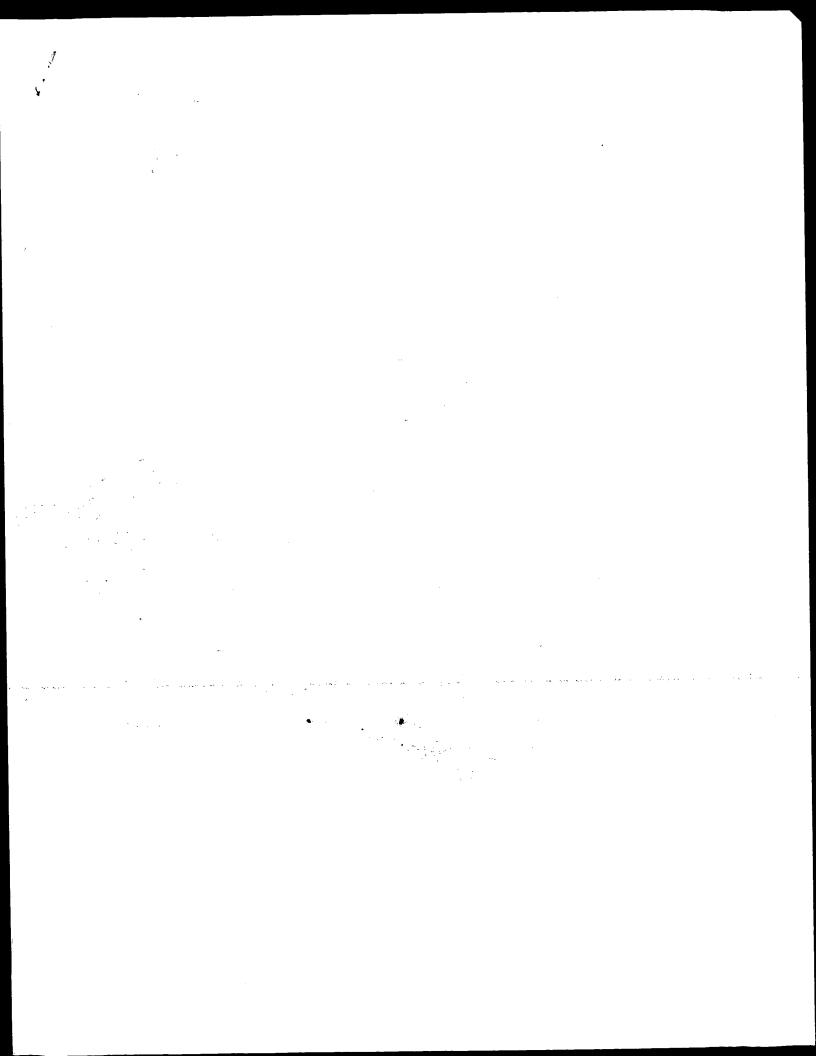
Conservative

89;

•	QY 177 LGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLS 218
•• 1	REMGMLAECI
··· • • • • • • • • • • • • • • • • • •	117
	EMPVTKKPRMAASSAGRIKGDELCVVCGDRASGYHYNALTCEGCKGFFRRSITKNAVYKC
••	116
	APAIPLHSAAAELASNHPRGPEANLEVRPKESWNHADFVHCEDTE
32	Query Match 18.6%; Score 463; DB 2; Length 469; Best Local Similarity 27.7%; Pred. No. 1.7e-28; Matches 137; Conservative 87; Mismatches 161; Indels 110; Gaps 18;
	C)166 37V/VOHMAIN: GIDA CRANSIORMING PROTEIN homology <erba></erba>
	10010
	A;Residues: 1-469 <for> A;Cross-references: GB:U18374; NID:q868031; PIDN:AAC52205.1; PTD:q868032</for>
	A:Status: preliminary; nucleic acid sequence not shown A:Molecule type: mRNA
	A) Reference number: A56918; MUID:95292336 A) Accession: A56918
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	C:Species: Rattus norvegicus (Norway rat) C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999
٠	ADDVID
	RESULT 15
	Db 432 KKLPPLLSETWDV 444
	Qy 456 IHPEATPLMQELEGI 470
Job time: 5357 sec	QY 398 HRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQD 455
Search completed: Februar	
	Qy 341 GRLSYCLED-TAGGEQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLESPDRPGVLQ 397
	Db 257 TELAIISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHETECIT 313
Qy 456 IHPFATPLMCELFGI	Qy 283 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC 340
399	Db 230DQPKVTPWPLGADPQSRDARQQRFAHF 256
Qy 399 RVVDQLQEQEAITLK	QY 223 LPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHM 282
Db 341 HADLLEERIRKSG	Db 187 PGTSEASSQGSGEGEGIQ-LTAAQELMIQQLVAAQLQCNKRSFS 229
QY 339 ECGRLSYCLEDTAGG	Qy 178GVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCE 222
Db 284 LTEMATSHVQIL	Db 127 FMRRKCQLCKLRKCKEAGMREQCVLSEEQIRKKKIQKQQQQQPPPPTEPASGSSARPAAS 186
Qy 279 LPHMADMSTYMFKGI	Qy 128 KTRROCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPL 177
268	Db 67 GPAPKMLGHELCRVCGDXASGFHYNVLSCEGCKGFFRRSVVHGGAGRYACRGSGTCQMDA 126
Qy 219 SGCELPESLÇAPSRE	QY 69 NADEEVGGPQICRVCGDKATGYHENVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITR 127
Db 219 EDSEGRDLRCVTSTI	Db 7 SLDTPLPGNGSPQPSTSSTSPTIKEEGQETDPPPGSEGSSSAYIVVILEPEDEPERKRKK 66

. DV 468 LKSYIECNRPO-PAHRFLELKIMAMLTELRSINAOHTORLL--RIOD 455 REEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSL 278 -----NKILKE----- 283 I 470

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/cDCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:*
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US-07-843-350C-10
US-07-843-350C-10
US-07-843-350C-10
US-07-843-350C-18-2
US-08-330-283-2
US-08-365-13931-2
US-08-365-13931-2
US-08-363-694-8
US-08-373-652-3
PCT-US95-1331-3
US-08-372-631-3
US-08-372-631-3
US-08-372-631-2
PCT-US95-16311-1
US-08-372-631-1
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Sequence 2, Appli	US-08-694-501-2	ب	548	14.9	371	5
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Sequence 2, Appli	US-08-333-358-2	,	548		371	ü
Sequence 2, Appli	US-08-465-375-2	ω	475	14.9	371	2
Sequence 2, Appli	US-08-484-200-2	N	475	14.9	371	ï
Patent No. 5260432	5260432-2	G	454	15.7	392.5	ö
Patent No. 5171671	5171671-2	σ	462	16.1	401	õ
	US-08-592-383-4	N	403	16.1	401.5	8
Patent No. 5223606	5223606-3	IJ	368	16.4	409	3
Sequence 2, Appli	PCT-US92-02320A-2	4	797	16.6	413	õ
Sequence 2, Appli	US-08-095-728B-2	N	797		413	ភ
Sequence 4, Appli	PCT-US92-02320A-4	4	462	16.6	413	4
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Sequence 2, Appl1	US-08-592-383-2	N	462	16.6	413	ຮັ
Sequence 2, Appl1	PCT-US94-07266-2	4	433	16.6	414.5	~
Seguence 2, Appli	US-08-466-120-2	N	433	16.6	414.5	ö
Patent No. 5438126	5438126-2	u	410	16.8	418	õ

ALIGNMENTS

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APPLICALL

FILING DATE:
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 00786/
REFERENCE/DOCKET NUMBER: 00786/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-08-459-489-10
US-08-459-489-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION NUMBER: US/08/459,489
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 348
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DAVID D. MOORE et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                TYPE: amino acid
STRANDEDNESS: N/I
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Query Match 30.8%; Score 768; DB 1; Length 348; Best Local Similarity 42.2%; Pred. No. 9.9e-69; Matches 164; Conservative 62; Mismatches 109; Indels

62; Mismatches

Indels 54;

Gaps

6

80 CRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLR 139

Best Local Similarity 42.2%;

Pred. No. 9.9e-69;

9

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Query Match
                                                                       US-08-458-686-10
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GENERAL INFORMATION:
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                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wodderfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" D1
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 LRSINEAYGYQIQHIQGLSAM-MPLLQEI 346
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                                                                                                              TYPE: amino acid
STRANDEDNESS: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PS, OPERATING SYSTEM:
                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                 348
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                                                                                                                                                                                                                                              (617) 542-8906
                                                                                            linear
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30.8%;

Score 768;

DB 1;

Length 348;

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US-07-843-350C-10
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GENERAL INFORMATION:
APPLICANT: David P
                                                                            REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SPQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 13 5" Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: David D. Moore et al. TITLE OF INVENTION: CAR RECEPTOR TITLE OF INVENTION: MOLECULES AN NUMBER OF SEQUENCES: 10
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  LENGTH: 3*c
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                                                                                                                                                                                             REGISTRATION NUMBER: 30,162
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STRANDEDNESS:
                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/843, FILING DATE: February 26, 1992
                                                                                                                                                                                                                        NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 KCLDAGMRKDMILSAEALALRRAKQAQRRAQQTPVQ-----LSKEQEELIRTLLGAHTR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CYVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPF-AGSCEVSKTQRRHCPACRLQ 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VLPLVTHFADINTFMVLQVIKFTKDLPVFRSLPIEDQISLLKGAA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Fish & Richardson
225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                   US/07/843,350C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 109;
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METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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linear

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US-07-737-736B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/07737736B Patent No. 5260199 GENERAL INFORMATION:
                  TELEFAX: 414-277-5774
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 164; Conservative
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Best Local Similarity
                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version $1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,736B
FILING DATE: 19910730
SEQUENCE CHARACTERISTICS:
                                                        NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 414-277-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DeLuca, Hector F.
APPLICANT: Ross, Troy K.
APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
                                                                                                                                                                        FILING DATE: 19910730
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 LRSINEAYGYQIQHIQGLSAM-MPLLQEI 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 YVLMQAISLESPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 VEICHIVLNTTFCLQTQNFLCGPLRYTIEDGARVGFQVEFLELLFHFHGTLRKLQLQEPE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 LRSINAQHTQRLLRIQDIHPFATPLMQEL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 FELCQLRENTYENAETGTWECGRLSYCLEDTAG-GFQQLLLEPMLKFHYMLKKLQLHEEE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 ------VLPLVTHFADINTFMVLQVIKFTKDLPVFRSLPIEDQISLLKGAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 SVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 TFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 KCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMK 199
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 CVVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPF-AGSCEVSKTQRRHCPACRLQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 CRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRROCQACRLR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVLLAAMALFSPDRPGVTQRDEIDQLQEEMALTLQSYIKGQQRRPRDRFLYAKLLGLLAE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milwaukee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 East Wisconsin Avenue
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42.2%; Pred. No. 9.9e-69;
ative 62; Mismatches 109; Indels 54; Gaps
                                                                                                        96-296-2185-2
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Sequence 2, Application US/08330518
Patent No. 5607967
GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
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APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
UNMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                350 NSMKLTPLVLEVFG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                           457 HPF-ATPLMQELFG 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 RVVDQLQEQFAITLKSYIECNRPQPAHRELELKIMAMLTELRSINAQHTQ--RLLRIQDI 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 SQDYKYDVTDVSKAGHTLELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 RLSYCLEDT---AGGFQOLLLEPMLKFHYMLKKLQLHESEYVLMQAISLFSPDRPGVLQH 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 LADLVSYSIGKVIGFAKMIPGFRDLTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 MADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCOLRFNTVFNAETGTWECG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 TLSFSGNSSSSSSDLYTTSLDMMEPSGFSNLDLNGEDSD-----DPSVTLDLSPLSMLPH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 GTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 RLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 25.2%; Score 629; DB 1; Length 367; Local Similarity 38.5%; Pred. No. 8.7e-55; hes 144; Conservative 70; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Burmester, James K.
AUTHORS: Maeda, No. 5260199uyo
AUTHORS: Detuca, Hector F.
TITLE: Isolation and expression of rat
TITLE: 1,25-dihydroxyvitamin D3 receptor cDNA
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
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DATE: February-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
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                                                                                                                                                                                Holloway, M. Katharine
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STREET: 126 F

COUNTRY: STATE:

New Jersey SD

07065-0907

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                   Sequence 2, Application US/08330283 patent No. 5679518
GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
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LENGTH: 461 amino acids
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TELECOMMUNICATION INFORMATION:
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  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 ---LTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 VLSEEQIRKKK--IRKQQQQESQSQSPVGPQGSSSSASGPGASPGGSEAGSQGSGEGE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 SYTRIKRPQDQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPPLLSEIWDV 459
                                                                                                                                                                                                                           414 SYIECNRPOPAHRELELKIMAMLTELRSINAQHTQRL--LRIQDIHPFATPLMQELEGI 470
                                                                                                                                                                                                                                                                                                                                                                                                                                            253
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STRANDEDNESS: sir
TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 YNVLSCEGCKGFFRRSVVRGGARRYACRGGGTCQMDAFMRRKCQQCRLRKCKEAGMREQC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 20.1%; Score 500.5; DB 1; Length Local Similarity 28.0%; Pred. No. 8.9e-42; Les 134; Conservative 93; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                         LQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPGRVEALQQPYVEALL 404
                                                                                                                                                                                                                                                                                                                                                           QVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECITFLKDFTYSKDDFHRAG
                                                                                                                                                                                                                                                                                                                                                                                                VISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC----GRLSYCLED-TAGG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                          P------LGAD-----PQSRDARQQRFA---HFTELAIISVQEIVDFAK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVQLTAAQELMIQQLVAAQLQCNKRSES------------DQPKVTPW 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQACRLRKCLESGMKKEM 150
                                                                                                                                                                                                                                                                                                                 FQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLK 413
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Friedman, Eitan
Holloway, M. Katharine
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; ANTI-SENSE: US-08-330-283-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rodan, Gideon
APPLICANT: Rutledge, Su Jane
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
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LENGTH: 461 amino acids
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                                                                                                                                                                                                                                           217 GVQLTAAQELMIQQLVAAQLQCNKRSFS------------DQPKVTPW 252
                                                                                                                                                                                                                                                                                  182 ---LTEEQRAMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKW 238
                                                                                                                                                                                                                                                                                                                             159 VLSEEQIRKKK--IRKQQQQESQSQSPVGPQGSSSSASGPGASPGGSEAGSQGSGEGE 216
345 LQVEFINPITEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPGRVEALQQPYVEALL 404
                                        354 FQQLULEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLK 413
                                                                                                                   299 VISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC----GRLSYCLED-TAGG 353
                                                                                                                                                                                                     239 SQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAK 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            92 FNYMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQACRLRKCLESGMKKEM 150
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126 East Lincoln Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release $1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,248
FILING DATE: 14-MAY-1996
CLASSIFICATION NUMBER: 08/330,283
PRIOR APPLICATION NUMBER: 08/330,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (908) 594-472
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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APPLICANT:
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REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19327
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Merck & C
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                                 159 VLSEEQIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSASGPGASPGGSEAGSQGSGEGE 216
                                                                 151 IMSDEAVEERRALIKRKKSERTGTQ---PLGVQG------
                                                                                                                                        92 FNYMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQACRLRKCLESGMKKEM 150
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                      99 YNVLSCEGCKGFFRRSVVRGGARRYACRGGGTCQMDAFMRRKCQQCRLRKCKEAGMREQC 158
                                                                                                                                                                              39 PGGPDPDVPGTDEASSACSTDWVIPDPEEEPERKRKKGPAPKMLGHELCRVCGDKASGFH 98
                                                                                                                                                                                                                 33 PRGPEANLE-VRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCGDKATGYH 91
                                                                                                                                                                                                                                                                  Local Similarity
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126 East Lincoln Avenue
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Schmidt, Azriel
Vogel, Robert
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                                                                                                                                                                                                                                                 20.1%; Score 500.5; DB 2; 28.0%; Pred. No. 8.9e-42; Live 93; Mismatches 153;
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   Matches 134; Conservative
                     Query Match
Best Local Similarity
                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                  TOPOLOGY: 11
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TELECOMMUNICATION INFORMATION:
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NAME: Quagliato, Carol S
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                                                                                                                     HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                           NAME: Quagliato, Carol REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 07065-0907
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                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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STREET: 12
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                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                        amino acid
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59 (908)
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126 East Lincoln Avenue
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Schmidt, Azriel
Vogel, Robert
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                   20.1%; Score 500.5; DB 4; 28.0%; Pred. No. 8.9e-42;
                                                                                                                                                                                                                                                                           594-3809
                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US95/13924
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93;
                                                                                                                                                                                                                                                                                                              19327
   Mismatches 153;
                                                                                                                                                                                                                                                                                                             PCT
   Indels 99;
                                 Length 461;
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 Gaps
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33 PRGPEANLE-VRPKESWNHADFYHCEDTESYPGKPSVNADEEVGGPQICRYCGDKAIGYH 91

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RESULT 9
PCT-US95-13931-2
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GENERAL INFORMATION:
                                                                                                                                      TELEPHONE: (908) 594-477
TELEFAX: (908) 594-477
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azziel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
      HYPOTHETICAL:
                        MOLECULE TYPE:
                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-3809
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                     NAME: Quagliato, Carol S. REGISTRATION NUMBER: 35,3
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19316 PCT
                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYTRIKRPODOLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPPLLSEIWDV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYIECNRPOPAHRELELKIMAMLTELRSINAOHTORL--LRIODIHPEATPLMOELEGI 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPGRVEALQQPYVEALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECITFLKDFTYSKDDFHRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC----GRLSYCLED-TAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSEEQIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSASGPGASPGGSEAGSQGSGEGE
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!NVLSCEGCKGFFRRSVVRGGARRYACRGGGTCQMDAFMRRKCQQCRLRKCKEAGMREQC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQACRLRKCLESGMKKEM 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGGPDPDVPGTDEASSACSTDWVIPDPEEEPERKRKKGPAPKMLGHELCRVCGDKASGFH
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: New Jersey
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                                                                                            461 amino acids
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126 East Lincoln Avenue
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Holloway, M. Katharine
. peptide
                                                                                                                                    594-4720
10 NO: 2:
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US-08-342-411A-2
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                      NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,928
REFERENCE, POCKET NUMBER: ARCD154
TELECOMMUNICATION INFORMATION:
                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
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                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 18-NOV-1994
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Sequence 2, Application US/08342411A Patent No. 5639616
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: 'Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR: TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LIAO, Shutsung APPLICANT: SONG, Ching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 SYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATPLMQELFGI 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 FQOLLLEPMIKFHYMIKKLQIHEEEEYVLMQAISLFSPDRPGVIQHRVVDQLQEQFAITLK 413 | : | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 77210-4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNVLSCEGCKGFFRRSVYRGGARRYACRGGGTCQMDAFMRRKCQQCRLRKCKEAGMREQC 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 4433
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28.0%; Pred. No. 8.9e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 461;
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US/08/342,411A

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                                                                                                                                                                                                                                                                                                                                                                                                             US-08-333-358-8
                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08333358
Patent No. 5571696
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.0%; Score 498; DB 1; Length 460; Best Local Similarity 27.4%; Pred. No. 1.6e-41; Matches 143; Conservative 87; Mismatches 154; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
                                                                                                                                                         APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGGERE Ph.D., VINCENT NMN
APPLICANT: YAO Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 KIMAMLTELRSINAQHTQRL--LRIQDIHPFATPLMQELFGI 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
                                    COUNTRY:
                                                                           CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPPLLSEIWDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLQLHEEEYVLMQAISLESPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFL 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQQQSQSQSQSPVGPQGSSSSASGPGASPGGSEAGSQGSGEGEGVQLTAAQELMIQQLVA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSERTGTQ---PLGVQG-------195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSTDWVIPDPEEEPERKRKKGPAPRMLGHELCRVCGDKASGFHYNVLDCEGCKGFFRRSV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KASTIEIMLLETARRYNHET---ECITFLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMR
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79-0924
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RESULT 12

US-08-463-694-8

Sequence 8, Application US/08463694

PATENT NO. 5696233

GENERAL INFORMATION: Ph.D., RONALD M.
APPLICANT: WANSELSDORF Ph.D., DAVID
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 440 amino acids
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NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                         431 LLSEIWDV 438
                                                                                                                                                                                                                                                                                                                                                                                                                   315 NREDFAKAGLQVEFINPIFEFSRANNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL
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                                                                                                                                                                                                                                                                                                 463 LMQELFGI 470
                                                                                                                                                                                                                                                                                                                                     375 QHTYVEALHAYVSIHHPH--DRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP
                                                                                                                                                                                                                                                                                                                                                                                 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 VSVQETVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 LPPRRSSPPQILPQLSPEQLGMIEKLVAAQQQCNRRSFS------------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/333,358 FILING DATE: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESL
                                                                                                                                                                                                                                                                                                                                                                QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---DRLRVTPWPMAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -HSGGHCPMCTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS
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314

Gaps

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US-08-463-694-8
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,068
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENEES: 14
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
ADDRESSEE: Pretty, Schroeder, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                            315 NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE------
463 LMQELFGI 470
                                               375 QHTYVEALHAYVSIHHPH--DRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP 430
                                                                                                                                                                                         346 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQL 404
                                                                                                                                                                                                                                                                                      288 YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFN--AETGTWECGRLSY 345
                                                                                                                                                                                                                                                                                                                                      228 QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 287
                                                                                                                                                                                                                                                                                                                                                                                                                                   185 LPPRRSSPPQILPQLSPEQLGMIEKLVAAQQQCNRRSFS------
                                                                                                                                                                                                                                       256 VSVQEIVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY 314
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 EDTESVPGKPSVNADEEVGGPQICKVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 19.7%; Score 491.5; DB 1; Length 440; Local Similarity 29.7%; pred. No. 6.6e-41; ndels 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/O FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEQFAITLKSYIECNRPQPAHRFLFLKIMAMUTELRSINAQHTQRL--LRIQDIHPFATP 462
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GIGUERE Ph.D., VINCENT NMN
YAO MT., TSO-PANG NMN
VENTION: NOVEL RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                              Matches 127;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Bh.D., ANTHONY E.
APPLICANT: GIGUREF Ph.D., UWE K.
APPLICANT: GIGUREF Ph.D., VINCENT NMN
APPLICANT: YAO.MI., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/761,068
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Relter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                 171 ---RIGTOPLGVOGLIEEQRMMIRELMDAQMKIFDTTFSHFKNFRLPGVLSSGCELPESL 227
                                                                                                                    128 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 184
                                                                                                                                                         117 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 170
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                68 EPTEIRPQKKKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGAHYIC 127
                                                                                                                                                                                                                                     57 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 116
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 287
                                      LPPRRSSPPQIILPQLSPEQLGMIEKLVAAQQQCNRRSFS----- 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 amino acids
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                                                                                                                                                                                                                                                                              19.7%; Score 491.5; DB 1; 29.7%; Pred. No. 6.6e-41; ative 85; Mismatches 145;
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                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FENGTH: 447 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
135 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 191
                      117 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IDENTIFICATION OF A DISTINCT
TITLE OF INVENTION: RETINOID-RESPONSIVE PATHWAY AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mangelsdorf, David APPLICANT: Willy, Patricia J.
                                                                           75 EPTEIRPQKRKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGAHYIC 134
                                                                                               375 QHTYVEALHAYVSIHHPH--DRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Reiter, Stephen REGISTRATION NUMBER: 3
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                                                                                                                                                                        Match 19.7%; Score 491.5; DB 1; Local Similarity 29.7%; Pred. No. 6.7e-41;
                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 9007]
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                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/373,935
                                                                                                                                                    85; Mismatches 145; Indels 71; Gaps
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US-08-372-652-3
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US-08-372-652-3
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        Query Match
Best Local Similarity
Matches 125; Conserv
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                                                                                                                                                                                                                                                                                NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDICH TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Moore, David
APPLICANT: Sec1, Wong1'
APPLICANT: Cho1, Hueng-Sik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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19.6%; Score 490; DB 2; Length 446; 29.1%; Pred. No. 9.5e-41; tive 84; Mismatches 128; Indels
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Suite 3100
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Gaps

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435	LOOPYVEALLSYTRIKRPODOLRFPRMLMKLVSLRTLSSVHSEQVFALRLODKKLP 435	380	Б
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319	SVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLQTAR	263	뮹
344	MFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLS 344	289	δÃ
262	DQPKVTPWPLGADPQSRDARQQRFAHFTELAII 262	230	В
288		229	VΩ
229	ASSQGSGEGEGIQLTAAQELMIQQLVAAQLQCNKRSFS	192	용
228	KNFRLPGVLSSGCELPESLQ	177	õ
191	LCRLRKCKEAGMREQCVLSEEQIRKKRIQKQQQQQPPPPSEPAASSGRPAASPGTSE	134	В
176	ACRLRECLESGMEKEMIMSDEAVEERRALIEREKESERTGTQP 176	135	Ϋ́
133	74 GHELCRVCGDKASGFHYNVLSCEGCKGFFRRSVVHGGAGRYACRGSGTCQMDAFMRRKCQ	74	용
134	76 GPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ	76	υ

Search completed: February 18, 2001, 14:31:59 Job time: 6202 sec

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

Y25411 standard; Protein; 473 AA.

Human nNR7-1 protein. 06-SEP-1999 (first entry)

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identification; downstream target gene; cell proliferation;
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Claim 20; Fig 6; 80pp; English.
                                                                                         DNA encoding human nuclear receptors nNR7 and nNR7-1
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N-PSDB; X78808.
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12-DEC-1997;
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RESULT Y15936
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                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                   treatment.
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Best Local Similarity
                                                                                                              A human intranuclear receptor protein
                                               Homo sapiens.
                                                                           treatment.
                                                                                       Human; intranuclear
                                                                                                                                           04-AUG-1999
                                                                                                                                                                                            Y15933 standard;
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N-PSDB; X59974.
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                                                                                                                                                                                                                                                          421 PQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFGITGS 473
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7.3e-237;
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Matches 473
Human; vitamin D receptor related protein; VDRR; obeanorexia; rheumatoid arthritis; lipoprotein defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human intranuclear receptor profile nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment of various diseases.
                             Human vitamin D receptor related gamma 2 protein.
                                                                  Y09516
                                                                                   Y09516 standard; Protein; 473
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  obesity; diabetes;
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14-OCT-1997;
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                SYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLLE
                                                                                                                                    SVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRK 120
                                                                                                                            svpgkpsvnadeevggpqicrvcgdkatgyhfnvmtcegckgffrramkrnarlrcpfrk
                                                                                        gaceitrktrrqcqacrlrkclesgmkkemimsdeaveerralikrkksertgtqplgvq
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240 180

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polypeptide. Human VDRR polypeptides and substances which affect VDRR c signal transduction, can be used for treating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a cc medicament for treating the following conditions: obesity, diabetes, can one can be used in the manufacture of a cc medicament for treating the following conditions: obesity, diabetes, can orexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and conditions in the capable of vectors encoding for expression of a VDRR polypeptide can be used for treating metabolic, proliferative or inflammatory conditions, capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or cantagonist can be used for the manufacture of a medicament for treating metabolic, proliferative or inflammatory condition.

ON N.B. The specification specifically claims the VDRR nucleic acid and condition of the specification in figures 1, 4, 7 and 8, but no figures to the condition of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a human vitamin D receptor related (VDRR) polypeptide. Human VDRR polypeptides and substances which affect signal transduction, can be used for treating metabolic, prolifer
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                   FSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNY
fshfknfrlpgvlssgcelpeslqapsreeaakwsqvrkdlcslkvslqlrgedgsvwny
                                    gmkkemimsdeaveerralikrkksertgtqplgvqglteeqrmmirelmdaqmktfdtt
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98.7%;
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Pred. No. 3.8e-221;
1; Mismatches 5;
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                                                                                                     Query Match
Best Local (
                                                                                             Matches
                                                                                                                                                           The present sequence represents a human intranuclear receptor property acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment of various diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         A human intranuclear receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y15932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1999
                                                                                                                                            Sequence
                                                                                                                                                                                                                     Claim 2; Page 16-17; 38pp; Japanese.
                                                                                                                                                                                                                                      New intranucleat receptor protein - useful for diagnosis and treatment of disease
                                                                                                                                                                                                                                                                    N-PSDB; X59967
                                                                                                                                                                                                                                                                                                                 11-AUG-1997;
                                                                                                                                                                                                                                                                                                                                    07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                      18-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                         JP11127872-A.
                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; intranuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y15932 standard:
                                                                                                                                                                                                                                                                                              (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                               treatment.
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                                                                                                    Match 93.6%;
Local Similarity 98.7%;
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                                                                                                                                                                                                                                                                             1999-350330/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQA 384
GMKKEMIMSDFAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTT
                 sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISLESPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 AA;
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                 97JP-0230335
                                                                                                                                                                                                                                                                                                                                    98JP-0224172
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                                                                                            Score 2334; DB 20;
Pred. No. 3.8e-221;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                       protein; drug development; diagnosis;
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                                                                                                                Length 457;
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             This invention describes the isolation of the novel human nuclear receptors nRR7 or nRR7-1. The nRR7 and nRR7-1 proteins are useful in the identification of downstream target genes and ligands regulating its activity. The nuclear receptor is involved in the regulation of in vivo cell proliferation and/or cell development. The nRR7 and nRR7-1 polynucleotides, expression vectors and host cells are useful for the recombinant production of the protein.
 Sequence
                                                                                                          Claim 1; Fig 3; 80pp; English.
                                                                                                                           DNA encoding human nuclear receptors nNR7 and nNR7-1
                                                                                                                                                       N-PSDB;
                                                                                                                                                               WPI; 1999-405024/34.
                                                                                                                                                                                        Chen F;
                                                                                                                                                                                                                                 14-OCT-1998;
12-DEC-1997;
                                                                                                                                                                                                          (MERI ) MERCK 6
                                                                                                                                                                                                                                                                 11-DEC-1998;
                                                                                                                                                                                                                                                                                                            W09931129-A1
                                                                                                                                                                                                                                                                                                                                                          nNR7; nNR7-1; nuclear trans-acting receptor protein; human; regulator; identification; downstream target gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                       24-JUN-1999
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                               Human nNR7 partial protein.
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                                                                                                                                                                                                                                                                                                                                                     development.
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                                                                                                                                                       X78807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 AA;
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97US-0069401.
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Query Match Best Local Similarity

93.6%;

Score 2334; DB 20; Pred. No. 3.9e-221;

Length 466;

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RESULT 8
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The present sequence represents a human intranuclear receptor protein. The nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment of various diseases.
                                                                                   New intranuclear receptor protein - useful for drug development diagnosis and treatment of disease % \left\{ 1,2,\ldots ,n\right\}
                                                                Claim 1; Page 15-16; 38pp; Japanese.
                                                                                                                           N-PSDB;
                                                                                                                                   WPI; 1999-350330/30.
                                                                                                                                                            (NISB ) JAPAN TOBACCO
                                                                                                                                                                                  11-AUG-1997;
                                                                                                                                                                                                         07-AUG-1998;
                                                                                                                                                                                                                               18-MAY-1999.
                                                                                                                                                                                                                                                                                                     Human; intranuclear receptor protein; drug development; diagnosis;
                                                                                                                                                                                                                                                                                                                                A human intranuclear receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 DKATGYHENVMTCEGCKGEFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLES 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 aknlppssprgpeanlevrpkeswnhadivhcedtesvpgkpsvnadeevggpqlcrvcg 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AAELASNHPPGPEANLEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCG
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Sequence

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                                                                                                                                                                Human; vitamin D receptor related protein; VDRR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia; hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour; hyperproliferative skin disorder; hyperthyroidism.
                                                                                                                                                                                                                                                                     Y09515 standard; Protein; 437
                                                                                                                                                                                                                Human vitamin D receptor related gamma protein.
                                                                                                                                                                                                                                 16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                           31-AUG-1998;
                                                                                                                               W09919354-A1
                                                                                                                                                 Homo sapiens.
                                                              31-MAR-1998;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; X56242
         WPI; 1999-302508/25
                           Berkenstam A,
                                            (PHAA ) PHARMACIA & UPJOHN AB
                                                                                                                                                                                                                                                                                                                421 atplmgelfgitgs 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCELPESIOAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEE 159
                                                                                                                                                                                                                                                                                                                                                                                                                              phmadmstymfkgiisfakvisyfrdlpiedqisllkgaafelcqlrfntvfnaetgtwe
                            Dahlberg M;
                                                                98SE-0001148.
97SE-0003745.
                                                                                           98WO-SE01548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.8%; Score 2289; DB 20;
100.0%; Pred. No. 9.5e-217;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 434;
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New vitamin D receptor related (VDRR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis

Claim 19; Page 19-20; 35pp; English.

The present sequence is a human vitamin D receptor related (VDRR) polypeptide. Human VDRR polypeptides and substances which affect VDRR signal transduction, can be used for treating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a medicament for treating the following conditions: obesity, diabetes, anorexia, lipoprotein defects, hyperlipidaemia, hyperchaperotalizamia and osteoporosis, rheumatoid arthritis, benign and hyperlipoproteinsemia and osteoporosis, rheumatoid arthritis, benign and malign tumours, hyperproliferative skin disorders or hyperthyroidism. Nucleic acid vectors encoding for expression of a VDRR polypeptide can be used for treating metabolic, proliferative or inflammatory conditions, be used for treating a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or antagonist can be used for the manufacture of a medicament for treating metabolic, proliferative or inflammatory condition.

N.B. The specification specifically claims the VDRR nucleic acid and polypeptide sequences given in figures 1, 4, 7 and 8, but no figures are given in the specification.

Sequence 437 AA;

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                      460 ATPLMQELFGITGS 473
                                            361 vvdqlqeqfaitlksyiecnrpqpahrflflkimamltelrsinaqhtqrllriqdihpf
                                                           400 VVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPF
                                                                                                                 340 CGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHR 399
                                                                                                                                         241 phmadmstymikgiisfakvisyfrdlpiedqisllkgaafelcqlrfntvfnaetgtwe
                                                                                                                                                    280 PHMADMSTYMFKGIISFAKVISYFRDLÞIEDQISLLKGAAFELCQLRFNTVENAETGTWE 339
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421 atplmgelfgitgs
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                   1 mevrpkeswnhadfvhcedtesvpgkpsvnadeevggpq1crvcgdkatgyhfnvmtceg 60
                                                                                                                                                                                      RRALIKRKKSERTGTOPLGVOGLTEEQRAMIRELADAQAKTFDTTFSHFKNFRLPGVLSS
                                                                                          Conservative
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RESULT 10 Y21799

Y21799 standard; Protein; 434 AA

14-SEP-1999 (first entry)

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CC SXR (steroid and xenoblotic receptor). SXR (1) forms a heterodimer with CC retinoid x receptor (RXR), (11) binds to a direct or inverted repeat CC transcription through response element motif based on the half-site AGTTCA, (11) activates CC transcription through response elements present in steroid-inducible P450 CC genes, in response to a wide variety of natural and synthetic steroid CC demonses and (10) is prominently expressed in liver and intestine. SXR CC regulates expression of catabolic enzymes, in response to many different CC steroids, and thus affects metabolism. SXR is a broad specificity, low-CC affinity receptor for reducing excessive levels of steroids in the CC circulation. (Ant)agonists of SXR are used to regulate metabolism of CC cases of tuberculosis (treated with rismpin and related compounds), in cases of tuberculosis (treated with tamoxifen, raloxifen etc.), or osteoporosis (treated with steroid levels are excessive (e.g. cc labsylaroxiase deficiency, or breast, colorectal or prostatic ovarian (cc dehydrogenase deficiency, or breast, colorectal or prostatic cancer), while antagonists are used where endogenous steroid levels are too low. CC clis that express SXR are used to identify compounds likely to be involved in undesirable drug interactions. Antibodies specific for SXR ante used in the present sequence represents SXR polypeptide.
                                                                                Query Match
Best Local Similarity
Matches 416; Conserv
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                                                                                                                                                                                                                                                                                   Sequence
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40 LEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEG 99
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95.9%;
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                                                                                                                      Score 2171;
Pred. No. 3
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                                                                            mismatches 16;
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GENERAL SERVICE SERVIC

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The invention provides an isolated human nuclear receptor (designated pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase (CYP) promoter. The hPXR is used to identify: its specific modulators, and compounds that induce CYP3A4 expression (i.e. to identify drug interactions, since CYP3A4 is involved in many biotransformations of drugs). The modulators are potentially useful for: associating particular

diseases and

conditions

treating such

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New human pregnane X^{\text{T}} receptor, used to identify specific modulators and agents that induce expression of cytochrome P-450 mono-oxygenase -
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Claim 4; Fig 1A-D; 69pp; English.
                                                                                                                    WPI; 1999-601202/51.
                                                                                                                                                          Kliewer SA, Willson TM;
                                                                                                                                                                                                                                                                                                                       30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human pregnane X receptor (hPXR).
                                                                                                                                                                                                                                     27-MAR-1998;
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Best Local
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                                                                                                                                                                                                                  Y42689;
        WPI; 1999-601202/51
                         Kliewer SA,
                                                           27-MAR-1998;
                                                                            26-MAR-1999;
                                                                                             30-SEP-1999.
                                                                                                              W09948915-A1
                                                                                                                                Homo
                                                                                                                                        Synthetic
                                                                                                                                                       Human; nuclear receptor; pregnane X receptor; PXR; cytochrome P-450 mono-oxygenase; drug interaction;
                                                                                                                                                                                 His6-pregnane X receptor (PXR) sequence
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                                                                                                                                                                                                                                    Y42689 standard; Protein; 316
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401 atplmgelfgitgs 414
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                                         GLAXO GROUP LTD
                         Willson TM;
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95.48;
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Pred. No. 8.8e-205;
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                                                                                                               Key
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                                     WO9622390-A1
                                                                           Domain
                                                                                                  Domain
                                                                                                                                     Xenopus laevis
                                                                                                                                                               hydroxybenzoate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apsreeaakwsqvrkdlcslkvslqlrgedgsvwnykppadsggkeifsllphmadmsty 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mfkgiisfakvisyfrdlpiedgisllkgaafelcqlrfntvfnaetgtwecgrlsycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 1585; DB 20; ilarity 100.0%; Pred. No. 1e-147; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                           receptor 6; XOR-6; steroid receptor; e; mercaptobenzoate; aminobenzoate.
                                                                                                                                                                                                  receptor 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA,
                                                                                                  Location/Qualifiers 37..102
                                                                         /label= DNA_binding_domain
183..386
                                                              Ligand_binding_domain
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Best Local :
        Rat vitamin D receptor protein VDRO
                                                                                W94623
                                         29-APR-1999 (first entry)
                                                                                                            W94623 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        steroid receptor superfamily, characterised as being responsive to the presence of hydroxy, mercapto or amino benzoate(s) and as regulating the transcription of associated gene(s). It shows 73% identity in the DNA binding domain, and 42% identity in the ligand binding domain, to the human vitamin D receptor. Recombinant XOR-6 can be expressed in animal cells: a cDNA clone (T36499) coding for XOR-6 has been isolated. The recombinant XOR-6 may be used to regulate gene transcription or to raise antibodies of diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding receptor polypeptide responsive to hydroxy, mercapto amino benzoate(s) - useful to regulate gene transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 27-28; 42pp; English.
                                                                                                                                                                                       328 fidsgrppspgnrllypkimecitelrtvndihskglleiwdigpdatblmrevfg
                                                                                                                                                                                                                     415 YIECHR-PQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFG 469
                                                                                                                                                                                                                                                                268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus orphan receptor 6 (XOR-6) (R98521) is a new member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blumberg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SALK ) SALK INST BIOLOGICAL STUDIES.
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                                                                                                                                                                                                                                                                                                                                                               296
                                                                                                                                                                                                                                                                                                                                                                                                                        236 AKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHWADMSTYMFKGIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 PFRKGACEITRKTRRQCOACRLRKCLESGMKKEMIMSDEAVEERRALIKRK-KSERTGTQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 eeeedasnscgtgededdgdpk1cracgdratgyhfnamtcegckgffrravkrn1r1sc 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutic appln.
                                                                                                                                                                                                                                                                                    QQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKS 414
                                                                                                                                                                                                                                                                                                                     fakmlpyfksldiedqiallkgsvaevsvirfntvfnsdtntwecgpftydtedmflagf 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pf-qnscvinksnrrhcqacrlkkcldigmrkelimsdaaveqrralikrkhkltklppt 132
                                                                                                                                                                                                                                                      rqlfleplvr1hrmmrklnvqseeyammaals1fasyrpgvcdwek1qklqeh1altlkd
                                                                                                                                                                                                                                                                                                                                                      FAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT-AGGF 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ppga-sltpeqqhfltqlvgahtktfdfnftfsknfr------pir--- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996-354546/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                         ------rssdpt---qepqats--seaflmlphisdlvtymikgiis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0374445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 979.5; DB 17; 48.6%; Pred. No. 5.1e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Umesono K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes rat vitamin D receptor (VDR) isoform protein VDR1. The present egguence represents rat VDR0. VDR1 differs from the canonical form of VDR (VDR0) by lacking the amino acid sequence encoded by exon 9, but instead substitutes a short sequence (GTEPGREELRDIGHYGDCE in the rat protein) encoded by the 5'-end of intron 9. VDR1 has a dominant negative effect on the vitamin D signalling pathway. The isoform protein can be used for determining bone density, and for the screening of compounds (e.g. steroids and retinoic acid derivatives) for vitamin D activity (e.g. as bone calcium regulators, immunosuppressants or anticancer agents).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
370 pgshqlyakmiqkladlrslneehskqyrslsfqpensmkltplvlevfg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 47pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene for vitamin D receptor isoform protein which blocks vitamin D signal pathway - and production of recombinant isoform protein using t, for bone density assay and for screening compounds for vitamin
                                   423 PAHRELELKIMAMLTELRSINAOHTO--RLLRIODIHPE-ATPLMOELEG
                                                                                                 363 LKFHYMLKKLOLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQ 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vitamin D receptor; VDR; bone density; retinoic acid derivative;
                                                                                                                                                                   306 LPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSYCLEDT---AGGFQQLLLEPM
                                                                                                                                                                                                                                                                                                     197 QMKTEDTTFSHFKNFRLPGVL---SSGCELPESLQAPSREEAAKWSQVRKDLCSLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUS ) CHUGAI SEIYAKU
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                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOCAL
                                                                                                                                   ltsddqivllkssaievimlrsnqsftmddmswdcgsqdykydvtdvskaghtleliepl
                                                                 1kfqvglkkln1heeehvllmaicivspdrpgvqdaklveaiqdrlsntlqtyircrhpp
                                                                                                                                                                                                   psgfsnldlngedsd-----dpsvtldlsplsmlphladlvsysiqkvigfakmipgfrd
                                                                                                                                                                                                                                                                   hhktydptyadfrdfrppvrmdgstgsyspr----ptlsfsgnssssssdlyttsldmme
                                                                                                                                                                                                                                                                                                                                                                       RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 196
                                                                                                                                                                                                                                                                                                                                                                                                         pricgvcgdratgfhfnamtcegckgffrrsmkrkalftcpf-ngdcritkdnrrhcqac 79
                                                                                                                                                                                                                                                                                                                                                                                                                                           POICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 136
                                                                                                                                                                                                                                     ----SLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRD
                                                                                                                                                                                                                                                                                                                                         rlkrcvd1gmmkef11tdeevqrkrem1mkrkeeealkds1rpk-1seeqqh11a111da
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone calcium regulator; immunosuppressant; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 801; DB 20;
Pred. No. 2.1e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 423;
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Matches 172;
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; vitamin D receptor; isoform protein; VDR1; VDR0; diagnosis; dominant negative receptor; signal transmission channel; bone density disorder; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W47509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W47509 standard; Protein; 423 AA.
                                                                                                                                                                                                                                                                                                                                               A novel cDNA sequence encodes the rat vitamin D receptor isoform protein (YDR1). The isoform differs from the normal receptor (YDR0), which comprises the present sequence, in having the vitamin D response element curtailed by 86 residues, and having an extra 19 residues inserted at the C-terminal of this element. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a vitamin D receptor isoform protein - useful for bone density determination and for screening substances for vitamin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V03129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-051917/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 46pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHUS ) CHUGAI PHARM CO LTD (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                             The isoform protein can be used to diagnose bone density disorders, and screen for substances having potential vitamin D-like activity.
                                                                                                                                                                                                                                                                                                                         transmission channel.
                                                                                                                                                                                                                                                                                                                                     acts as a dominant negative receptor in the vitamin D signal
251 ----SLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRD 305
                                                    197 QMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAPSREEAAKWSQVRKDLCSLKV---- 250
                                                                                                              137
                                                                                                                                                      77 POICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 136
                                                                                                                                          21
                                                                                                           RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 196
                                                                                                                                       pricgvcgdratgfhfnamtcegckgffrrsmkrkalftcpf-ngdcritkdnrrhcqac 79
                           Ueno K;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                             32.0%; Score 798; DB 19; illarity 42.0%; Pred. No. 4.2e-70; Conservative 74; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96JP-0194179
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                                                                                                                                                                                                                            Length 423;
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Search completed: February 18, 2001, 14:29:40 Job time: 8217 sec

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red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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BE266478 601192748 BE410116 601302405 BE275249 601122072 BE877201 601485121 BE897042 60128523 BE791424 601582443 BE791424 601582443 BE791424 601582449 AM505439 UI-HF BNO BE664197 148449 MA A1098643 us2f10.y BE303050 ba72h10.y BE303050 ba72h10.y BE315476 601664976 BE390515 601284134 AA570939 v185f05.r BE30317 60167713 AV609965 AV609965 BE385638 601278159 AA277757 vb09h11.r AA1124058 mc29081.r AA124058 mc29008.r AB233123 uc39912.y BE233303 139430 MA	39698 10796 12383 13938 26498	AV10857 AV10857 AV10857 AV10857 AW158294 za39e07.x AW107536 u191a06.y AI768052 w146b06.x BE573696 601333441 AW012320 um07d07.y AI004299 uc85h08.y AI004259 uc85h08.y	7469 7469 7737 7737	Description AV651714 AV651714 AA699679 zi78c07.s

ALIGNMENTS

ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AV651714	RESULT 1
Homo sapiens,	human.	EST.	AV651714.1 GI:9872728	AV651714 .	AV651714 GLC Homo sapiens cDNA clone GLCCSG03 3', mRNA sequence.	AV651714 638 bp mRNA EST 07-SEP-2000	•	

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This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
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1 (bases 1 to 638)
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/clone="GLCCSG03"
/clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
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461 TAGCCTGCTGGGGGTATACAGCATTGACTCAGATATAGATCCTGAGCTCACAGAGTTTA 402

Matches

458;

Similarity 99.1 58; Conservative

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Indels

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AUTHORS
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ORGANISM
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Wash T., Wash T., Froject Unpublished (1997)
Contact: Wilson RK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           z178c07.sl Soares_fetal_liver_spleen_lNFLS_S1 Homo clone IMAGE:446892 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
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314 286 1810
                                                                                                                             constructed by Bento Soares and M.Fatima Bonaldo."
1 126 c 86 g 131 t
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                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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99.1%;
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Score 445.2; DB 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N94132.1 (
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 454)

1 Hillier_L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project
                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N94132 454 bp mRNA EST za25g06.rl Soares fetal liver spleen INFLS image:293626 5', mRNA sequence.
                                                                                                                                                                                       IMAGE Consortium (info@image.linl.gov) for
Seq primer: mob.REGA+ET
High quality sequence stop: 416.
                                                                                                                                                                                                                    This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
/organism="Homo sapiens"
/db_xref="GDB:3801473"
/db_xref="taxon:9606"
/clone="IMAGE:293626"
                                                                             /sex="male"
                                                                                           /clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:1266441
                                                                  /dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                                                                                                      Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens cDNA clone
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1905 agatcccactaaagtgtcaaggtgtgggaagggaccaaggaccaaggataggccatctgg 1964
                        2323 aacaaacagahacacaaacaatttggat 2350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggtctatgcc:acatacccacgtttgttcgcttcctgagtcttttcattgctacctctaa 2024
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AACAAACAGAAACACAAACAATTTGGAT 454
                                                                                         GGGTATACAGCATTGGACTCAGATATAGATCCTGAAGCTCACAGAGTTTATAGTTAAAAA
                                                                                                                                                                                  CTGTGTCTCTGCATCCATTTGAACACATTATTAAGCACCGATAATAGGTAGCCTGCTGTG
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Pred. No. 3.9e-86;
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CCESSION AI746915 794 bp mRNA EST 22-JUN-1999
EFINITION U109a10, y1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE: 2076282 5' similar to TR:O54915 O54915 PREGNANE X RECEPTOR.
CCESSION AI746915.1 GI:5125179
EFRSION AI746915.1 GI:5125179
EYNORDS EST.
OURCE Mus mouse mouse.
ORGANISM EST.
EURAryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus musculus
EFERENCE 1 (Dases 1 to 794)
AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Duderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Persor, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
JORRAL Montact, Marra M. Washon, R.
Waterston, R. and Wilson, R.
TITLE The Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tal: 314 286 1810
Email: mouseest@watson.wustl.edu
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BASE COUNT
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agcggatgatgatcagggagctgatggac 747
                                                                          cccggaagacccggcgacagtgccaggcctgccgcctgcgcaagtgcctggagagcggca 598
                                                                                                                                                                                                                                                                                                                                999ccatgaaacgcaacgcceggctgaggtgccccttccggaagggcgcctgcgagatca 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccagtgtcaacgcagatgaggaagtcoggaggtcoccaaatctgccgtgtatgtggggaca 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaagctggaaccatgctgactttgtacactgtgaggacacagagtctgttcctggaaagc 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agaacttaccaccaagcagtccaagaggcccagaagcaaacctggaggtgagacccaaag 298
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                                               GGAAGAAGAGGGAANAGATTGAGGCTCCACCGCCTGGGAGGCANGNGCTGACGGAAGAAC 765
                                                                                                                                        TGAAGAAAGAGATGATCATGTCCGATGCCGCTGTGGAGCAGAGGCGGGCCTTGATCAAGA 705
                                                                                                                                                                                                                                    CCCGGAAGACACGACGCCAGTGCCAGGCCTGCCGTTTGCGCAAGTGCCTGGAGAGTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggccactggctatcacttcaatgtcatgacatgtgaaggatgcaagggctttttcagga 478
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                                                                                                                                                                      tgaagaaggagatgatcatgtccgacgaggccgtggaggagaggggccttgatcaagc 658
                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCCAATGGCTACCACTTCAATGTCATGACGTGTGAAGGATGCAAGGGGTTTTTCAGAA 525
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone_lib="Sugano mouse embryo mewa"
//dev_stage="embryo, 14 dpc"
//lab_host="PH108"
//lab_host="PH108"
//note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand CDNA was primed
with an oligo(dT) primer [ATGTGGCGTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CGACCTGCAGCTCGAGCACA."
06 a 180 c 253 g 152 t 3 others
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/db_xref="taxon:10090"
/clone="IMAGE:2076282"
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                                                                                                                                                                         315
                                                                                                                                                                                                             435 cttcaatgtcatgacatgtgaaggatgcaagggctttttcaggagggccatgaaacgcaa 494
                                                                                    375 tgaggaagtcggaggtccccaaatctgccgtgtatgtggggacaaggccactggctatca
                                                                                                                                         283 TGACTTTGTACACTGTGAGGACACAGAGTCTGTTCCTGGAAAGCCCAGTGTCAACGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 766 AGCAAGCGCIGATCCCAGAGCTGATGGAC 794
                                                                                                                                                                                                                                                                                        Local Similarity
nes 343; Conserv
                                                                                                                                                            tgactttgtacactgtgaggacacagagtctgttcctggaaagcccagtgtcaacgcaga 374
CTTCAATGTCATGACATGTGAAGGATGCAAGGGCCTTTTTCAGGAGGGCCATGAAACGCAA
                                                                   TGAGGAAGTCGGAGGTCCCCAAATCTGCCGTGTATGTGGGGACAAGGCCACTGGCTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI248626 343 bp mRNA EST 01-DEC-19 qh77b12.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens clone IMAGE:1850887 3' similar to gb:J03258 VITAMIN D3 RECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 343)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMAN); mRNA sequence. AI248626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI248626.1 GI:3844023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 338.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lnFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1850687"
                                                                                                                                                                                                                                                                                     11.8%; Score 343; DI
100.0%; Pred. No. 3.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                      3.4e-69;
                                                                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                                                                                                        Length 343;
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                                                                                                                                                              Matches
                                                                                                                                                                               Query Match
Best Local Similarity
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                  2413 ctgtgatggcaggcactgggtacccaagtgaaggttcccgaggacatgagtctgtaggag 2472
                                                                                                     2354 aaggagaaaatgataagtgacaaaagc-agcacaaggaatttccctgtgtgggatgctgag 2412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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305 CTGTGATGGCGGGCACTGGGTACCCAAGTGAAGGTTCCCGAGGACATGAGTCTGTAGGAG
                                                                              365 AAAGGAGAAATGATAAGTGACAAAAGCNACCACAAGGAATTTCCCTGTGTGGATGCTGAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCCCGGCTGAGGTGCCCCTTCCGGAAGGGCCCTGCGAAGATCACCCGGAAGACCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAGTGCCAGGCCTGCCGCCAAGTGCCTGGAGAGCGGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgcccggctgaggtgccccttccggaagggcgcctgcgagatcacccggaagacccggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 279.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N69311 365 bp mRNA EST 13-MAR-1996
za25g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
IMAGE:293626 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                  95
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                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                  double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatina Bonaldo."

a 106 c 68 g 95 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:293626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares fetal liver spleen lNFLS"
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/db_xref="GDB:3801473"
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                                                                                                                                                                            11.5%;
97.0%;
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Primates;
                                                                                                                                                              0
                                                                                                                                                            Score 335; DB 143;
Pred. No. 2.5e-67;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                              Indels
                                                                                                                                                                                                    Length
                                                                                                                                                            <u> 1</u>2
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RESULT
AA277370
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA277370 472 bp mRNA EST 01-APR-1997 va81a12.rl Soares mouse NML Mus musculus cDNA clone IMAGE:737758 similar to TR:G410518 G410518 ORPHAN NUCLEAR RECEPTOR OF STEROID/THYROID SUPERFAMILY. ;, mRNA sequence.

AA277370:

AA277370:1 GI:1917850
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; THACE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                           vector to vector length is 506 Seq primer: -28ml3 rev2 ET from
                                                                                                                                                                                                                                                                                                                                                      MGI:454806
                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                 Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases:1 to 472)
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:737758"
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                          organism-"Mus musculus"
                                                                                                                                                   host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowles, M., Dietrich, N., Dubuque, T
                                                                                                                                                                                                                                                                                                 Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                         information.
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RESULT
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ORGANISM
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ORIGIN
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                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
1 (bases 1 to 493)
1 (bases 1 to 493)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person, B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                       WashU Xenopus EST project,
Unpublished (1999)
Other_ESTs: da94c06.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
AW871811
                                                                                                                                                                               Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashLngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
address: www.rzpd.de)
Seq primer: -40RP from Gibco
High quality sequence stop: 4
                                                    Library constructed by B. Korn PhD. and S. Henze DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the RessourcenZentrumPrimarDatenbank, Berlin, Germany (web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW871811.1 GI:8005864
                                                                                                                                               Tel: 314 286 1800 Fax: 314 286 1810
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            African clawed frog.
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pus laevis tadpole stage 24 Xenopus laevis cDNA
similar to gb:J03258 VITAMIN D3 RECEPTOR (HUMA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tatcacttcaatgtcatgacatgtgaagggatgcaaggggctttttcaggagggccatgaaa 489
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                                                                                                                                                                                                                                                                                                                                               AA679591 200 bp mRNA EST 19-DEC-1997 2749612:s1 Soares_fetal_liver_spleen_lnFLS_S1 Homo sapiens cDNA clone IMAGE:453623 3' similar to TR:G410518 G410518 ORPHAN NUCLEAR RECEPTOR OF STEROID/THYROID SUPERFAMILY. ;, mRNA sequence.

AA679591
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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a 142 c 131 g 91 t
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/dev_stage="stage 24"
/lab_host="DH10B"
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/db_xref="taxon:8355"
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                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                    553 cgacagtgccaggcc 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 CACTTCAATGTCATGACATGTGAAGGATGCAAGGGCTTTTTCAGGAGGGTTATGAAACGC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 cacttcaatgtcatgacatgtgaaggatgcaagggctttttcaggagggccatgaaacgc 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 gatgaggaagtcggaggtccccaaatctgccgtgtatgtggggacaaggccactggctat 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 GATGAGGAAGTCGGAGGTCCCCAAATCTGCCGTGTATGTGGGGGACAAGGCCACTGGCTAT 141
                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                            80 AACGCCCGGCTGAGGTGCCCCTTCCGGAAGGGCGCCTGCGAGATCACCCGGAAGACCCCGG
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                                                                                                                                                                                                                                                                                                                                            CGACAGTGTCCAGGC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    aacgcccggctgaggtgccccttccggaagggcgcctgcgagatcacccggaagacccgg 552
                                                                                                                                            AW511148 463 bp mRNA EST 03-MAR-2000 hd22a05.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR ; mRNA sequence.
                                                                                                        EST
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-WCI human EST Project Unpublished (1997) Contact: Wilson RK
Mammalia; Eutheria;
1 (bases 1 to 463)
                                                                                                                          AW511148.1 GI:7149226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 154.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver spleen; Site_1: pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
Liver spleen lNFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:453623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="20 week-post conception fetus"
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96.9%;
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Pred. No. 1.2e-32;
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JOURNAL COMMENT
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AV108557
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TITLE
                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 gtatgtggggacaaggccactggctatcacttcaatgtcatgacatgtgaaggatgcaag 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 gttcctggaaagcccagtgtcaacgcagatgaggaagtcggaggtccccaaatctgccgt 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 GTGAGACCAAAGGAAAGCTGGAACCATGCTGACTTTGTACACGTGAGGACACAGAGTTCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 gtgagacccanagaaagctggaaccatgctgactttgtacactgtgaggacacagagtct 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTATGTGGGGACAAGGCCACTGGCTATCACTTCAATGTCATGACATGTGAAGGATGCAAG
Malludid, Durant, Color, Malludid, Marting, Malludid, Marting, Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV108557 215 bp mRNA EST 28-JUN-1999 AV108557 Mus musculus liver C57BL/6J 13-day embryo Mus musculus CDNA cloue 2510047D01, mRNA sequence.
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Email: Robert_Strausberg@nih.gov
This clone is available royalty-
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV108557:1 GI:5256105
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for further information. Seg primar: -400P from Gibco
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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//lab_host="bH108"
//note="Corgan: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729996-731399. Subtraction by Bento Soares and M. Fattma Bonaldo. "
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/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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91.7%;
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Pred. No. 3.8e-28;
0; Mismatches 16
                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                       AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       acgaggccgtggaggagggcgggccttgatcaag 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggcctgccgcctgcgcaagtgcctggagagcggcatgaagaaggaggatgatcatgtccg 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGCTGCCCCTTTCGCAAGGGAACCTGCGAGATCACCCGGAAGACACGACGGCAGTGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgaggtgcccttccggaagggcgcctgcgagatcacccggaagacccggcgacagtgcc 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTGACCCGTGCAGGATGCAGGGCCTTTTTCAGCAGGCCCCTGACACACAATGTCCGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCCTGCCGTTTGCGCAAGTGCCTGGAGAGTGGCATGAAGAAGAGATGATAATGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184;
Expressed sequence tags from Xenopus Unpublished (1999)
                                                   Xenopodinae; Xenopus.

1 (bases 1 to 432)

Schutz,K., de la Bastide,M., Huang,E.N., Nascimento,L., Preston,I
                                                                                                                                                                                 Xenopus laevis
                                                                                                                                                                                                                                                                                             za39e07.x1 Xenopus EST library Xenopus laevis cDNA clone za39e07
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                AW158294.1 GI:6270323
                                                                                                                                                                                                                                                                                                                                 AW158294
                                                                                                                                                                                                       African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
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/dev_stage="l3-day embryo"
60 c 69 g 38
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/clone="2510047D01"
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/strain="C57BL/6J"
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85.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | C99C9aCa9t9Cca99cCt9Cc9CCt9C9Caa9t9CCt9GagagagC9GCatgaagaaggag 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGATCATGTCCGATGCAGCGGTGGAACAGAGACGAGCGCTAATTAAG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgcaacgcccggctgaggtgccccttccggaagggcgcctgcgagatcacccggaagacc 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCGCCACTGCCAGGCCTGTCGGCTCAAGAATGTCTGGACATCGGCATGAGGAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatcacttcaatgtcatgacatgtgaaggatgcaagggctttttcaggagggccatgaaa 489
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 601) Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                           AW107536 601 bp mRNA EST 20-OCT-1999
u191a06.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2159410 5' similar to gb:03258 VITAMIN D3 RECEPTOR (HUMAN
gb:U15548 Mus musculus beta 2 thyroid hormone receptor (MOUSE);,
                                                                                                                                                                                                                                         EST
                                                                                                                                                                                          Mus musculus
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Plate: za39 row: e column: 07
Seq primer: M13 universal forward
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                                                                                                                                                                                                                                                            AW107536.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector: Lambda Zap I; Site_1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs). cDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50-56 tadpoles, total brain tissue, GTC extraction method."

8 90 c 142 g 88 t
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/tissue_type="total brain tissue
/cell_line="W22-TGA"
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/db_xref="taxon:8355"
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Local Similarity 64.3%;
                                                                                                                                                                                                                                                                                            gtggaggagaggcgggccttgatcaagcggaagaaaagtgaacggacagggactcagcca 690
                                                                                                                                                                                                                                                                                                                                                            CGGCTCAAACGCTGCGTGGACATTGGCATGATGAAGGAGTTCATCCTCACAGATGAGGAG 423
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CACCACAAGACCTACGACCCCACCTATGCCGACTTCCGGGACTTGCTGCCTCCA 594
                                                                                                                                                                 ctgggagtgcaggggctgacagaggagcagcggatgatgatcagggagctgatggacgct 750
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                                                                                                                                                                                                                                        GTGCAGCGTAAGCGAGAGATGATCATGAAGAGGAAGGAGGAAGAAGACGCCTTGAAGGACAGT 483
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Other ESTS: u191a06.x1
Contact: Maarra M/MashU.NCI Mouse EST Project 1999
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Location/Qualifiers
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//lab_host="DHIOB"
//lab_host="DH
                                                                                                                    GCCCAAGCTGTCTGAGGAGCAACAGCACATTATCGCCATCCTGCTCGATGCC
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/sex="female"
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/db_xref="taxon:10090"
/clone="IMAGE:2159410"
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388 CCCCGGATCTGTGGGGTGTGGGAGACCGAGCCACTGGCTTTCACTTCAATGCTATGACC 329
                                                                                                                                                                                                                                                                                                                                                                                                                              391 ccccaaatctyccgtgtatgtggggacaaggccactggctatcacttcaatgtcatgaca 450
                                                                                                                                                                   511 cccttccggaägggcgcctgcgagatcacccgggaagacccggcgacagtgccaggcctgc 570
                                                                                                                                                                                                                                                                                                                     451 tgtgaaggatgcaagggctttttcaggagggccatgaaacgcaacgcccggctgaggtgc 510
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                                                                                                                          CCCTTC---AACGGGGACTGCCGCATCACCAAGGACAACCGACGCCACTGCCAGGCCTGC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 560)
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Seq primer: -40UP from Gibco
High quality sequence stop: 355.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. rel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"organ: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; plasmid DNA from the normalized library NCI_CGAP_Colo was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co16"
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                     451 tytyaagyatycaagygytttttcayyagyyccatyaaacyccaacycccygctgagytyc 510
                                                                      147 CCTCGGATCTGTGGAGTGTGTGGAGACCGAGCCACGGGCTTCCACCTTCAACGCTATGACC 206
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM8934 row: a column: 11

High quality sequence stop: 685.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1033)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="TAMAGE:3710866"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                            /note-"Organ: mammary; Vector: pCMV-SPORT6; Size_1: Sal1; Size_2: Not1; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

3 62 c 274 g 173 t
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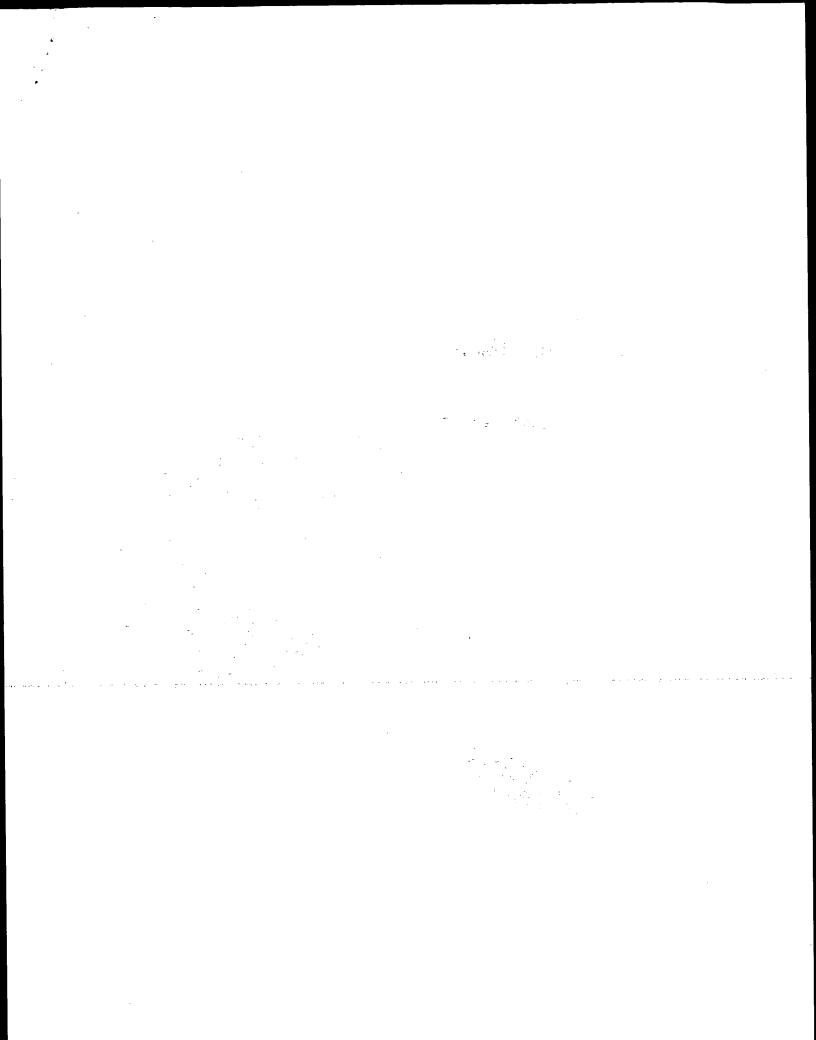
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                                                                                                                     cgcctgcgcaagtgcctggagagcggcatgaagaa-ggagatgatcatgtccgac-gagg 628
                                                                                                                                                                                                                                            CCCTTC---AATGGAGATTGCCGCATCACCAAGGACAACCGGCGACACTGCCAGGCCTGC 323
CCCACCACAAGACCTACGACCCCACCTATGCCGACTTCCGGGACTTCCGGCCTCCA
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US-08-372-652-7
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US-07-737-736B-5
US-08-459-489-1
US-08-459-686-1
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PCT-US93-01559-1
US-08-342-411A-1
US-08-342-411A-1
US-08-30-283-1
US-08-30-283-1
PCT-US95-13924-1
PCT-US95-13924-1
PCT-US95-13924-1
PCT-US95-128B-3
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Sequence 14, App	Sequence 14, App	Patent No. 543812	Sequence 11, App	Sequence 11, App	Sequence 11, App	Sequence 21, App	Sequence 19, App	Sequence 17, App	Patent No. 5260432	Sequence 1, Appl	Sequence 1, Appl	Sequence 2, Appl	Sequence 1, Appl	Sequence 7, Appl	Sequence 7, Appl	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-07-737-736B-6
                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6:
SEQUEENCE CHARACTERISTICS:
LENGTH: 2043 base pairs
TYPE, NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/07737736B Patent No. 5260199
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APPLICANT: Deluca, Hector.F.

APPLICANT: Ross, Troy K. ...

APPLICANT: Prahl, Jean M.

TITLE OF INVENTION: Method Of Producing

TITLE OF INVENTION: 1,25.Dihydroxyvitamin D3 Receptor Protein

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS: 6

ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/737
FILING DATE: 19910730
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
REFERENCE/DOCKET NUMBER: 96-2
TELECOMMUNICATION INFORMATION:
TELEFAX: 414-277-5715
TELEFAX: 414-277-5774
                  PUBLICATION INFORMATION:
AUTHORS: Burmester, James K.
AUTHORS: Wiese, Russell J.
AUTHORS: Maeda, No. 5260199uyo
AUTHORS: DeLuca, hector F.
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STREET: Milwaukee
CITY: Milwaukee
STATE: Wisconsin
T S.A.
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Rat
                                                                                                                                                                                         MOLECULE TYPE: ci
                                                                                                                                                                         ANTI-SENSE: NO
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TITLE: Structure and regulation of the rat
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TITLE: 1,25-dihydroxyvitamin D3 receptor JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

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Best Local Similarity 55.6%;
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1276 ctgcagctgcatgaggaggagtatgtgctgatgcaggccatctccctcttctccccagac 1335
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DATE: December-1988
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                               GCTGGGCACACCCTGGAGCTGATCGAGCCCCTCATAAAGTTCCAGGTGGGGCTGAAGAAG
                                                             ggtggcttccagcaacttctactggagcccatgctgaaattccactacatgctgaagaag 1275
                                                                                                                                                            CTTAAGTCAAGCGCCATTGAGGTGATCATGTTACGCTCCAACCAGTCTTTCACCATGGAT
                                                                                                                                                                                                                             GGCTTTGCCAAGATGATCCCAGGATTCAGGGATCTCACCTCCGATGACCAGATTGTCCTG
                                                                                                                                                                                                                                                                                         CCTCTCTCCATGCTGCCCCACCTGGCTGACCTTGTCAGTTACAGCATCCAAAAGGTCATC
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Pred. No. 2.9e-53;
0; Mismatches 482;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/07/737,736B
FILING DATE: 19910730
CLASSIFICATION: 435
CCLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Applica Patent No. 5260199
                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DeLuca
           AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 414-277-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1049
                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: double
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CITY: Milwaukee
STATE: Wisconsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Schwartz, Carl R. REGISTRATION NUMBER: 29,437
                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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RS: Hughes, Mark
RS: Crisp, Tracey M.
RS: Mangelsdorf, David J.
RS: Haussler, Mark R.
RS: Pike, J. W.
RS: Shine, John
RS: O'M:lley, Bert W.
Cloning and expression of encoding human vitamin D
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                                                                                                                                                               McDonnell, Donald
Hughes, Mark
                                                                                                                                                                                                    Baker, Andrew R
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             of full-length cDNA
D receptor
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Proc. Natl. Acad. Sci. U.S.A. 85

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; JOURNAL: Proc. Nat
; VOLUME: 85
; PAGES: 3294-3298
; DATE: May-1988
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Best Local Similarity 55.1%;
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1264 atgctgaagaagctgcagctgcatgaggagtatgtgctgatgcaggccatctccctc 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   590 GTGAATGATGGTGGAGGGAGCCATCCTTCCAGGCCCAACTCCAGACACACTCCCAGCTTC 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 cgcctgcgcaagtgcctggagagcggcatgaaggagagatgatcatgtccgacgaggcc 630
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                                                                            gaagacactgcaggtggcttccagcaacttctactggagcccatgctgaaattccactac 1263
                                                                                                                                                                     ttcaacgcggagactggaacctgggagtgtggccggc-----tgtcctactgcttg 1203
                                                                                                                                                                                                             CAGATEGTACTGCTGAAGTCAAGTGCCATTGAGGTCATCATGTTGCGCTCCAATGAGTCC 949
                                                                                                                                                                                                                                        cagatetecetgetgaagggggeegetttegagetgtgteaactgagatteaacacagtg 1152
                                                                                                                                                                                                                                                                                        CAAAAGGTCATTGGCTTTGCTAAGATGATACCAGGATTCAGAGACCTCACCTCTGAGGAC
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                                                          GACGTGACCAAAGCCGGACACAGCCTGGAGCTGATTGAGCCCCCTCATCAAGTTCCAGGTG 1069
                                                                                                                                   TTCACCATGGACGACATGTCCTGGACCTGTGGCAACCAAGACTACAAGTACCGCGTCAGT 1009
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Pred. No. 5.4e-52;
0; Mismatches 487;
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; Sequence 1, Application US/08459489
; Patent No. 5686574.
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 07/843,350
APPLICATION NUMBER: 07/843,350
FILING DATE: Pebruary 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T Clark
REGISTRATION NUMBER: 00,162
REFERENCE/DOCKET NUMBER: 00786/1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                   Matches
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: David D. Moore et al.

TITLE OF INVENTION: CAR RECEPTORS AND RELATED

TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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739 CTCTGGTCACACTTCGCAGACATCAACACTTTCATGGTACTGCAAGTCATCATGTTA 798
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                              992 ccctgctgccccacatggctgacatgtccaacctacatgttcaaaggcatcatcagctttg 1051
                                                                                        / Match 5.9%; Score 170.6; DB 1; Local Similarity 57.5%; Pred. No. 3.3e-29; has 327; Conservative 0; Mismatches 239;
                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Massachus
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/459,489 FILING DATE: .
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NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
TELEFAX: 2001.54
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08458686 Patent No. 5710017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: David
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                                                                                                                                                                                                                                            COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                 APPLICATION NUMBER: 07/843,350 FILING DATE: February 26, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     979
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                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                   CLASSIFICATION: 514
                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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225 Franklin Street
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VENTION: CAR RECEPTORS AND RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULES AND METHODS
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Best Local (
                                                                                                                                                                                                                                                                    Sequence 1, Application US/07843350C Patent No. 5756448
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: David
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        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Ps/2 Model 50% or 558X
OPERATING SYSTEM: IBM P.C. DOS (Version
                                                                                                                                                                                                  APPLICANT: David D. MOOTE et al.
TITLE OF INVENTION: CAR RECEPTOR
TITLE OF INVENTION: MOLECULES AN
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TYPE: nucleic acid
STRANDEDNESS: sing
                                                                         STATE: Massachus
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                       STREET: 225,1
CITY: Boston
                                                                                                                                                         ADDRESSEE:
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225, Franklin Street
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AND RELATED METHODS

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1279 TGTCTGCCATGATGCCGCTGCTCCAGGAG
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GENERAL INFORMATION:

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Hest Local Similarity 57.5%;
Matches 327; Conserve+4...
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY_AGENT INFORMATION:

NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 0078

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEPAX: (617) 542-8906
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PRIOR APPLICATION DATA:
                                                                                                                                    1469
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STRANDEDNESS: single
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TETCTGCCATGATGCCGCTGCTCCAGGAG 1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 170.6; DB 1; Length 1450; Pred. No. 3.3e-29; 0; Mismatches 239; Indels 3;
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PCT-US93-01559-1 RESULT Sequence 1, Application PC/TUS9301559

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: FEDRUARY 26, 199
ATTOREY AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IEM PS/2 Model 502 or 558X
OPERATING SYSTEM: IEM P.C. DOS (Version 3.30)
SOFTWARE: WcrdPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: David D. TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1450
                                                                                                                                                                                                                                                                                                       1172
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                                                                                      1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1052 ccaaagtcatctcctacttcagggacttgcccatcgaggaccagatctccctgctgaagg 1111
1099 CCCAGAGAGATGAGATTGATCAGCTGCAAGAGGAGATGGCACTGACTCTGCAAAGCTACA
                        1349 tgcagcaccgcgtggtggaccagctgcaggagcaattcgccattactctgaagtcctaca 1408
                                                                                                                                                                     979 TAGAGTTTTTGGAGTTGCTCTTTCACTTCCATGGAACACTACGAAAACTGCAGCTCCAAG 1038
                                                                                                                                                                                                                                                                                                                                                  859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          739 CTCTGGTCACACACTTCGCAGACATCAACACTTTCATGGTACTGCAAGTCATCAAGTTTA 798
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STREET: 22
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                              aacttctactggagcccatgctgaaaattccactacatgctgaagaagctgcagctgcatg 1288
                                                                                                                                                                                                                                                                                     cctgggagtgtggccggctgtcctactgcttggaagacactgcaggt---ggcttccagc 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTRAGGACCTGCCGTCTTCCGTTCCCTGCCCATTGAAGACCAGATCTCCCTTCTCAAGG
                                                                                                          aggaggagtatgtgctgatgcaggccatctcccctcttctccccagaccgcccaggtgtgc 1348
                                                                                                                                                                                                                                                            ACTTCCTCTGCGGGCCTCTTCGCTACACAATTGAAGATGGAGCCCGTGTGGGGTTCCAGG 978
                                                                                                                                                                                                                                                                                                                                                GAGCAGCTGTGGAAATCTGTCACATCGTACTCAATACCACTTTCTGTCTCCAAACACAAA 918
                                                                                      Boston
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CAR RECEPTORS AND RELATED MOLECULES
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US-08-342-411A-1
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US-08-342-411A-1
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Best Local Similarity 47.6%;
Matches 585; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,92
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APPLICATION NUMBER: US,
FILING DATE: 18-NOV-19:
CLASSIFICATION: 435
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CORRESPONDENCE ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 tgccccttccggaagggcg---cctgcgagatcacccggaagacccggcgacagtgccag 564
                                                                                 448 acatgtgaaggatgcaagggctttttcaggagggccatgaaacgccaggcccggctgagg 507
                                                                                                                                                     388 ggtccccaaatctgccgtgtatgtggggacaaggccactggctatcacttcaatgtcatg 447
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                                                          374 GACTGCGAAGGCTGCAAGGGCTTCTTCCGGCGCAGTGTGGTCCGTGGTGGGGCCAGGCGC 433
                                                                                                                                   314 GGCCACGAGCTTTGCCGTGTCTGTGGGGACAAGGCCTCCGGCTTCCACTACAACGTGCTC 373
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                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tacacccctttgctacgcccctcatgcag 1557
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                                                                                                                                                                                                           Score 97.6; DB 1;
Pred. No. 6.9e-13;
0; Mismatches 569;
                                                                                                                                                                                                                                                Length 1898;
                                                                                                                                                                                                           Indels 76;
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1449 AGTGAGGGGCTGGCCACCCAGCCCACAGC 1478
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### CASTGCCCCTGCCCTCCCCCCCCCCCCCCCCCCCCCCCCC																																
494 CASTGGGGCTGGGGAATGGAATGGAAAAGGGTGGGAAAGAAGGAGCAAGTCAAGTCACAGTGGAAAAGTCACAGTGGAAAAGAATGGAAAAAGAATGGAAAAAGAATGGAAAAAGAATGGAAAAGAATGGAAAAAGAATGGAAAAAGAATGGAAAAAGAATGGAAAAAGAATGGAAAAAGAATGGAAAAGAATGGAAAAGAAG	·. } .	Q 5		, Db Vy	Db Db	Db 43	₽ B	Qy	Д	Qγ	Db	γQ	ממ	γQ	Db .5	Q 5	, 4g) B	у	40	ОУ	Db	Оу	ДD	Qy	מם	Qy	ממ	γΩ	da da	Оу	dd Db
gegitegegecigegeagggegetetagaagaggagaagattagatcatgtcogacagacagagagagagatgattagatcatgtcogacagagagagagagagagagagagagagagagagaga	1440	1577	1517	1457 1335	1397 1275	1215	מ ב	1277	1095	1217	1035	1163	975	1103	915	1043	א מ מ	803	923	743	865	683	805	667	745	614	685	554	625	494	رب د	434
				ш ц			GGCCTGGACGACGCTGAGTACGCCCTGCTCATCGCCTCAACATCTTCTCGGCCGGC	tgcagctgcatgaggaggagtatgtgctgatgcaggccatctccctcttctccccagacc 133	CAGGCCTGCAGGTGGAGTTCATCAACCCCATCTTCGAGTTCTCGCGGGCCATGCGGGGC	giggoticcagcaactictactggagcccatgctgaaattccactacatgctgaagaagc 127	AGACAGAGTGTATCACCTTCTGAAGGACTTCACCTACAGGAAGGA	agactggaacctgggaqtqtqqccqqctqtcctactqcttqqaaqacactgcaq	TCCTGAAGGC/TCCACTATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAACCACG	tyctgaagggygccgctttcgagctgtgtcaactgagattcaacacagtgttcaacgcgg	TGGACTTCGCTAAGCAAGTGCCTGGTTTCCTGCAGCTGGGCCGGGAGGACCAGATCGCCC	0.11000001.11011.11011.01011.1100001.100001.1001.11000.11000.11000	agarciroscoryongospanasaspanasaspanasaspanasaspanasaspanasaspanasaspanasaspanasaspanasaspanasaspanasaspanasaspa 	CAGCCCAAAG!!CACGCCCTGGCCCCTGGGCGCAGACCCCCAGTCCCGAGATGCCCGCCAG 86	tgcggggggaggatgtctggaactacaaacccccagccgacagtggcgggaaag	CTAATGATCCAGCAGTTGGTGGCGCCCCAACTGCAGTGCAACAAACGCTCCTTCTCCGAC	gctgccaagt;gagccaggtccggaaagatctgtgctctttgaaggtctctctctgcagc	GAGGCAGGCAGGCTCCGGGGAAGGAGGGTGTCCAGCTAACAGCGGCTCAAGAA	ggggtgcttagcagtggctgcgagttgccagagtctctgcaggccccatcgagggaagaa	TTCCCCTGGTGGATCT 6	gacgotoagatgaaaacotttgacactacottotoccatttcaagaatttccggotgcca	CAGTCACCTGTGGGGCCCAGGGCAGCAGCTCAGCCTCTGGGCCTGGGGC 6	cagocactgggagtgcaggggctgacagaggagcagcggatgatgatcagggagctgatg 7	GAACAGATCCGGAAGAAGAAGATTCGGAAACAGCAGCAGCAGCAGTCACAGTCACAGTCG 6	gaggccgtggaggagaggcgggccttgatcaagcggaagaaaagtgaacggacagggact 6	CAGTGCCGGCTGCGCAAGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGTGCTTTCTGAA 55	gcctyccgccrycgcaagtgcctggagagcggcatgaagaaggagatgatcatgtccgac 6	4 TATGCCTGCC3GGGTGGCGGAACCTGCCAGATGGACGCTTTCATGCGGCGCAAGTGCCAG 493

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                                                                                                                                      Matches
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP6-2262:
FILING DATE: 21-SEPT-1994
APPLICATION NUMBER: PCT/JP95,
FILING DATE: 21-SEPT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: JP6-226270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
438 CCCCGAAGATGCTGGGCCACGAGCTTTGCCGTGTGTGGGGGACAAGGCCTCCGGCTTCC 497
                 374 atgaggaagtcggaggtccccaaatctgccgtgtatgtggggacaaggccactggctatc 433
                                                           378 CAGACTGGGTCATCCCAGATCCCGAAGAGGAACCAGAGCGCAAGCGAAAGAAGGACCCAG 437
                                                                                            314 ctgactttgtacactgtgaggacacagagtctgttcctggaaagcccagtgtcaacgcag 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAMURA, YUSUKE APPLICANT: : SAITO, HIROKO
                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 206..1591
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Kalamazoo
STATE: Michigan
                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                    LIBRARY:
                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                   Human mammary gland cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (616) 381-1156
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                                                                                                                                                                                                                                                                                                                                                                                     cDNA to mRNA
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                                                                                                                                                                                                                                    experimental examination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Furuya Case 1343
                                                                                                                                             Score 97.6; Db
                                                                                                                                    Mismatches
                                                                                                                                                                  DB 2; Length 1979;
                                                                                                                                 174;
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314 ctgactttgtacactgtgaggacacagagtctgttcctggaaagcccagtgtcaacgcag 373

Matches

215;

Conservative

Query Match Best Local Similarity

3.4%;

Score 97.6; DB 1; Pred. No. 7.1e-13; 0; Mismatches 174;

Length 2030;

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Gaps

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US-08-330-518-1
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                                                                                                                                                          TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO:
                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,518
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
                ANTI-SENSE:
                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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CLASSIFICATION: 435
                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                        CENGTH:
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                                                                                           TELEPHONE: (908) 594-428
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,502
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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HYPOTHETICAL:
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                        TOPOLOGY:
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Schmidt, Azriel
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Holloway, M. Katharine
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                    DNA (genomic)
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594-4720
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Patent No. 5939
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                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/330,28:

FILING DATE: 27-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dolan, Catherine A.

REGISTRATION NUMBER: 36,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schildt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 07065-0907
                                                                                                                                                                          APPLICATION NUMBER: US/08 FILING DATE: 14-MAY-1996
                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atgaggaagtcggaggtccccaaatctgccgtgtatgtggggacaaggccactggctatc 433
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126 East Lincoln Avenue
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Schmidt, Azriel
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Holloway, M. Katharine
Rodan, Gideon
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TELEPHONE:

(908) 594-4283

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  STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9513924
GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Rodan, Gideon
APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER.
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
HYPOTHETICAL: NO
ANTI-SENSE: NO
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Best Local Similarity 54.8%;
Matches 215; Conservative
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                                                                                                                                                                                                                                             E: Merck & Co., Inc.
126 East Lincoln Avenue
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PCT/US95/13924
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RESULT 13
PCT-US95-13931-1
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NAME: Quagliato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19327 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3809
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                               Sequence 1, Application PC/TUS9513931 GENERAL INFORMATION:
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                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co.,
                                                                                                                                                                  APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM
                                                                                                                                                                                                                                            APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
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LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL: NO
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                       STATE: New Jers
COUNTRY: US:
ZIP: 07065-0907
                                                                                STREET: 126 F
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Similarity 54.8%; Pred. No. 7.1e-13;
15; Conservative 0; Mismatches 174; Indels 3
                                                              New Jersey
                                                                                                     126 East Lincoln
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                                                                                                                                                              Sequence 3, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.4%;
Best Local Similarity 54.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Quagliato, Carol S.
REGISTRATION UNDER: 35,330
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DI
                                                                       CORRESPONDENCE ADDRESS:
                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 ctgactttgtacactgtgaggacacagagtctgttcctggaaagcccagtgtcaacgcag 373
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STREET:
CITY: H
STATE:
                                                                                                                                                                                                                                                                              777 CACAGTCACAGTCGCAGTCACCTGTGGGGCCG 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                      ADDRESSEE:
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Houston : Texas
                                                                                                                                                                                   Application PC/TUS9412883
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                                    P.O. Box 4433
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                                                      Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                          UBIQUITOUS NUCLEAR RECEPTOR: COMPOSITIONS AND METHODS
                                                                                            38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US95/13931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97.6; DB 4; Pred. No. 7.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2030;
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US-08-095-728B-3
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                                                                                     Sequence 3, Application US/08095728B Patent No. 5843642 
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEPAN: (713) 789-2679 TELEEA: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: PC APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Versi
SOFTWARE: #1.25
                                                       APPLICANT:
                                   APPLICANT:
                                                                         APPLICANT:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 ggtccccaaarctgccgtgtatgtggggacaaggccactggctatcacttcaatgtcatg 447
                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 TATGCCTGCCGGGGTGGCGGAACCTGCCAGATGGACGCTTTCATGCGGCGCAAGTGCCAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 tgccccttccggaagggcg---cctgcgagatcacccggaagacccggcgacagtgccag 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 GGCCACGAGCTTTGCCGTGTCTGTGGGGACAAGGCCTCCGGCTTCCACTACAACGTGCTC 288
                                                                                                                                                                                                                         529 CAGTCACCTGTGGGGCCG
                                                                                                                                                                                                                                                                 685 cagccactgggagtgcag 702
                                                                                                                                                                                                                                                                                                    469 GAACAGATCCGGAAGAAGAATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCG 528
                                                                                                                                                                                                                                                                                                                                    625 gaggccgtggaggaggggggggccttgatcaagcggaagaaaagtgaacggacagggact 684
                                                                                                                                                                                                                                                                                                                                                                                  409 CAGTGCCGGCTGCGCAAGTGCAAGGAGGCAGGGATGAGGGAGCAGTGCGTCCTTTCTGAA 468
                                                                                                                                                                                                                                                                                                                                                                                                      565 gcctgccgcctgcgcaagtgcctggagagcggcatgaagaaggagatgatcatgtccgac 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AGCTGCGAAGGCTGCAAGGGCTTCTTCCGGCGCAGTGTGGTGGTGGTGGGGGCCAGGCGC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 77210
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Local Similarity 58.8%;
nes 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 10-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acatgtgaaggatgcaagggctttttcaggagggccatgaaacgcaacgcccggctgagg 507
           WARRELL JR, RAYMOND P
MILLER JR, WILSON H
FRANKEL, STANLEY
                                                                       DMITROVSKY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version
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 METHODS FOR THE
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Pred. No. 8.3e-13;
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   DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1813;
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US-08-095-728B-3
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Best Local Similarity 50.8%;
Matches 302; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1350 gcagcaccgcgtggtggaccagctgcaggagcaattcgccattactctgaagtcctacat 1409
                                               1071 TGCGGAGACGGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGACCGCCAGGACCTGGA 1130
                                                                                                                                     1173 ct999agtgt---ggccggctgtcctactgcttggaagacactgcaggtggcttccagca 1229
                                                                                                                                                                                                                                                                                                                                                    1113 ggccgctttcgagctgtgtcaactgagattcaacacagtgttcaacgcggagactggaac 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                            1053 caaagtcatctcctacttcagggacttgcccatcgagggaccagatctccctgctgaaggg 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                               1230 acttctactggagcccatgctgaaattccactacatgctgaagaagctgcagctgcatga 1289
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728
FILING DATE: 21-JU-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Sing
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                         951
                                                                                                                                                                                                                                                                                                                                 891
                                                                                                                                                                                                                                                                                                                                                                                                             831 CAAGCAGCTGCCCGGCTTCACCACCCTCACCATCGCCGACCAGATCACCCTCCTCAAGGC 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       771 CCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGC 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             993 cctgctgcccacatggctgacatgtcaacctacatgttcaaaggcatcatcagctttgc 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: hrar alpha
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 103..14
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                          99a99a9tatgtgctgatgcaggccatctccctcttctccccagaccgcccaggtgtgct 1349
                                                                                                                                                                                                                               CATGACCTTCTCGGACGGGCTGACCCTGAACCGGACCCAGATGCACAACGCTGGCTTCGG 1010
                                                                                                                                                                                                                                                                                                                         TGCCTGCCTGGACATCCTGCGGATCTGCACGCGGTACACGCCCGAGCAGGACAC
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103..1488
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Pred. No. 2e-11;
0; Mismatches 281; Indels 12
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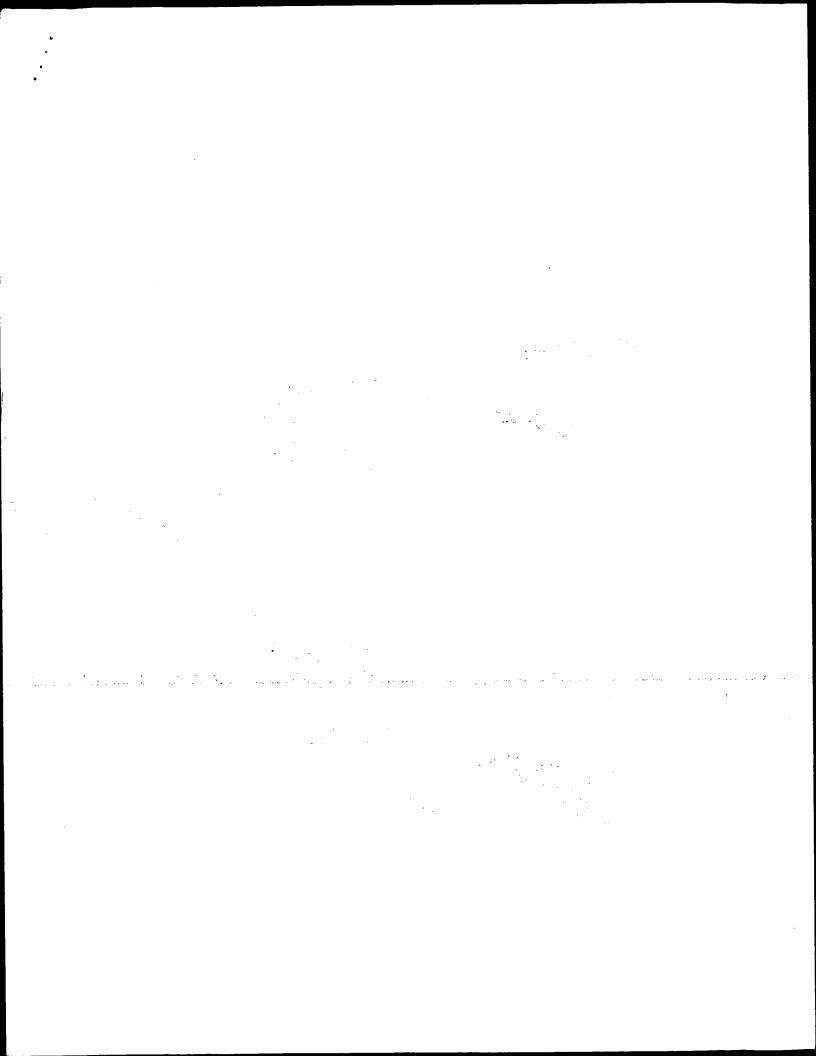
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                       1527 catacacccctttgctacgcccctcatgcaggagttgttcggcatcacaggtagc 1581
                                                                              1245 TACTGACCTCCGAAGCATCAGCGCCAAGGGGGGCTGAGCGGGTGATCACGCTGAAGATGGA 1304
                                                                                                                                                             1191 GCGGAAGCGCAGCCCAGCCCCCCACA-----TGTTCCCCAAGATGCTAATGAAGAT 1244
                                                                                                                                                                                                                                                    1131
                                                                                                        1470 caccgagctccgcagcatcaatgctcagcacaccccagcggctgct---gcgcatccagga 1526
                                                                                                                                                                                                   1410 tgaatgcaatcggccccagcctgctcataggttcttgttcctgaagatcatggctatgct 1469
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Search completed: February 18, 2001, 16:49:16 Job time: 8375 sec



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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         1110987654321
                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 2000000000
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1: /cgn2_2/gcgdt
2: /cgn2_2/gcgdt
3: /cgn2_2/gcgdt
4: /cgn2_2/gcgdt
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Match
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                                                                                                                                                                                                                                 Length DB
       2910
3093
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     X56242
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Human vitamin D re
Human nNR7 cDNA.
DNA encoding an in
DNA encoding an in
Human vitamin D re
Human nNR7-1 cDNA.
Human pregnane x r
Human steroid and
DNA encoding an in
DNA encoding an in
DNA encoding an in
SEQ ID 12 of JP111
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Human myı/kak-aıpn	V64990		3030	٥.٢	9.1¢
Human PML/RARalpha	V20474	9	3036	٠	91.4
ž	029334	ü	3036	ω Ļ	91.4
clone phRA	N90124	10	2940	•	91.4
alpha c	V64991	20	2928	•	91.4
RAR-alpha gene. S	Q29338	13	2928	•	91.4
tous	Q88760	16	1813	٠.	•
eceptor p	T30031	17	2030	.•	97.6
	T18996	17	2030	٠	٠
	Q63134	15	2030	•	٠
n foetal lung	T27616	17	1979	3.4	•
ncoding h	T79634	18	1898	. •	•
nucle	X80217	20	468	٠	٠
CAR	X24003	20	1361	•	٠
CAR	X23994	20	1450	٠	•
recep	Q46131	14	1450		•
titutively ac	T92305	18	1450	٠	•
	X80215	20	1280		•
encoding ra	V03130	19	1404	6.4	•
min.	X16597	20	1404	6. 5	•
ğ	X34790	20	1534	7.4	2
_	X16606	20	3382	8	236
A encoding	V18518	19	3382	ص نـز	ω
amin D re	X16596	20	1071	8.1	ω
us orphan re	T36499	17	2191	8.8	ū
vitamin D r	Q51424	14	1399	9.3	71.
vitamin D r	V41327	19	4604	9.4	72.
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e sequen	X34793	20	1574	•	72.
ide s	X34788	20	1463		72.
cleotide sequen	X34789	20	1382		72.
t vitamin Ď re	5142	14	2043	9.6	278.8
cDNA encoding rat	V03129	19	1960		7

ALIGNMENTS

THE STATE OF THE S Human; vitamin D receptor related protein; VDRR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia; hypercholesterclaemia; hyperlipoproteinaemia; osteoporosis; tumour; 31-MAR-1998; 14-OCT-1997; Berkenstam A, (PHAA) PHARMACIA & UPJOHN AB 31-AUG-1998; 22-APR-1999. WO9919354-A1 Homo sapiens. Human vitamin D receptor related gamma protein encoding cDNA 16-JUL-1999 (first entry) hyperproliferative skin disorder; hyperthyroidism; ss X56242 standard; cDNA; 2910 Dahlberg M; 98SE-0001148. 97SE-0003745. 98WO-SE01548 BP.

WPI; 1999-302508/25. P-PSDB; Y09515.

New vitamin D receptor related (VDRR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis

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The present sequence encodes a human vitamin D receptor related (VDRR) CC polypeptide. Human VDRR polypeptides and substances which affect VDRR CC signal transduction, can be used for treating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a comedicament for treating the following conditions: obesity, diabetes, anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or hyperlipipoprotein and osteoporosis, rheumatoid arthritis, benign and malign tumours, hyperproliferative skin disorders or hyperthyroidism.

CN Nucleic acid vectors encoding for expression of a VDRR polypeptide can be used for treating metabolic, proliferative or inflammatory conditions, by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or can be used for the manufacture of a medicament for treating content of the manufacture of a medicament for treating content of the proliferative or inflammatory condition.

CN N.B. The specification specifically claims the VDRR nucleic acid and content of the specification in the specification.
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                        Claim 10;
                                      New intranuclear receptor protein - useful diagnosis and treatment of disease
                                                              WPI; 1999-350330/30.
P-PSDB; Y16035.
                                                                                                                   07-AUG-1998;
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                                                                                                    11-AUG-1997;
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                     Page 35-37; 38pp; Japanese.
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sequence encodes acid sequence was
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X59974 Human; 04-AUG-1999 x59974; encoding intranuciear standard; an (first intranuclear DNA; entry) receptor ВÞ receptor

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treatment; SS protein; drug development; diagnosis;

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cc polypeptide. Human VDRR polypeptides and substances which affect VDRR CC signal transduction, can be used for treating metabolic, proliferative crimical contractions. They can be used in the manufacture of a cc medicament for treating the following conditions: obesity, diabetes, cc ancrexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or cc hyperlipoprotein aemia and osteoporosis, rheumatoid arthritis, benign and cc malign tumours, hyperproliferative skin disorders or hyperthyroidism. CC Nucleic acid vectors encoding for expression of a VDRR polypeptide can be used for treating metabolic, proliferative or inflammatory conditions, cc by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vivo and then polypeptide is expressed. CC antagonist can be used for the manufacture of a medicament for treating metabolic, proliferative or inflammatory condition. CC antagonist can be used for the manufacture of a medicament for treating cetabolic, proliferative or inflammatory condition. CC N.B. The specification specifically claims the VDRR nucleic acid and CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures care given in the specification.
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207997 standard; DNA; 2146 ВP

207997;

17-JAN-2000 (first

pregnane X receptor (hPXR) encoding

Human; nucl cytochrome nuclear receptor; pregnane X receptor; PXR; rome P-450 mono-oxygenase; drug interaction; CYP; CYP3A4; hPXR; ss.

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New steroid and xenobiotic receptor, used to identify modulators for controlling metabolism of steroids and xenobiotics, e.g. reducing
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                                        WPI; 1999-419349/35.
P-PSDB; Y21799.
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CC The invention relates to a novel nuclear receptor polypeptide, designated CC SXR (steroid and xenobiotic receptor). SXR (i) forms a heteroid mer with CC retinoid X receptor (RXR), (ii) binds to a direct or inverted repeat CC response element motif based on the half-site AGTTCA, (iii) activates CC transcription through response elements present in steroid-inducible P450 CC genes, in response to a wide variety of natural and synthetic steroid commones and (iv) is prominently expressed in liver and intestine. SXR CC regulates expression of catabolic enzymes, in response to many different controls, and thus affects metabolism. SXR is a broad specificity, low-cc affinity receptor for reducing excessive levels of steroids in the CC circulation. (Ant)agonists of SXR are used to regulate metabolism of catabolism of steroids particularly phytoestrogens or calcium-channel blockers, to reduce steroid toxicity in subjects being treated with steroids, e.g. in CC steroids particularly phytoestrogens or calcium-channel blockers, e.g. in CC cases of tuberculosis (treated with tamoxifen, raloxifen etc.) or osteoporosis (treated with vitamin K), or to-slow metabolism of therapeutic steroids. Also, modulating endogenous SXR is used to treat disease, particularly an agonist is used where endogenous steroid levels are excessive (e.g. CC cushing syndrome; virilism and hirsutism in women; polycystic ovarian CC dehydrogenase deficiency, or breast, colorectal or prostatic cancer), while antagonists are used where endogenous steroid levels are too low. CC clus that express SXR are used to identify compounds likely to be converted. The present sequence represents the longest SXR cDNA clone concerns the longest SXR cDNA clone encoding the SXR balverbulled.
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Sequence 2068 BP; 520 A; 541 C; 586 G; 420 T; 1 other;

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                                                                                                                                                                                                                                                                                                                                                                              New intranuclear receptor protein - useful diagnosis and treatment of disease
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P-PSDB; Y15933.
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ccatgaaacgcaacgcccggctgaggtgccccttccggaagggcgcctgcgagatcaccc
                                        ccactggctatcacttcaatgtcatgacatgtgaaggatgcaagggctttttcaggaggg
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                                                                                                                                                                                                                                                                                                        Claim
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P-PSDB; Y15931:
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                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                             Sequence 1960 BP;
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The isoform protein can be used to diagnose bone density disorders, and screen for substances having potential vitamin D-like activity
                                                                                                                                                                                 acts as a dominant negative receptor in the vitamin D signal
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                                                                                                                                                                                                                                                                                     activity
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant prodn. of 1,25-d1:hydroxy-vitamin-D3 - using expression system comprising insect cell recombinant virus contg. foreign DNA
                                                                                                                                                                                                                                                                                                         Sequence 2043 BP; 448 A; 647 C; 518 G; 430 T; 0 other;
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                                                  cycctycycaagtycctyyayayogycatyaagyayatyatcatytccyacyayycc
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X34789 standard; DNA; 1382 BP

06-JUL-1999 (first entry)

RESULT
X34789
ID X3
XX
AC X3
AC X3
AC X3
DT 06
XX
DE Nu
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KW V1
KW C0
XX
OS HO Vitamin D recept cofactor; human; Nucleotide sequence of human vitamin D receptor (VDR) gene transcript 9. receptor; VDR; hVDR; variant; isoform;

SRC-1;

GRIP-1; TFIIB;

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crofts LA,
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Pred. No. 6.2e-47;
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Search completed: February 18, 2001, 16:54:40 Job time: 8560 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Homo sapiens orphan nuclear
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AF084645.1 GI:3769538
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Mammalia; Eutheria; Primates
1 (bases 1 to 2905)
Bertilsson,G., Heidrich,J.,
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                                                                                     /product="orphan nuclear receptor"
/protein_id="AAC64558.1"
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/db_xref="GI"3769539"
/tanslation="MEVERKESWNHADEVHCEDTESVPGKPSVNADEEVGGPQICRVC
/translation="MEVERKESWNHADEVHCEDTESVPGKPSVNADEEVGGPQICRVC
GDXATGYHFNVMTCEGCKGFFRRAMKRNARLRCPPRKGACEITEKTRRQCQACRIRKC
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TFDTTFSHFKNFRLPGVLSSGCELPESLOAPSREEAAKWSQVRKDLCSLKVSLOLRGE
DGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLL
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
KGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQ
                                                                                                                                                                                                          /gene="PAR1"
/codon_start=1
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                     /gene="PAR1"
                                                                                                                                                                                                                                                                                                                                'tissue_type="liver"
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Eutheria; Primates;
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E14584 Rat mRNA is
U91846 Xenopus lae
AB037673 Paralicht
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AR009748 Sequence 1
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AF009327 Mus muscu
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                                                                                    CTGCAGGCCCCATCGAGGGAAGAAGCTGCCAAGTGGAGCCAGGTCCGGAAAGATCTGTGC
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h 727 c 778 g 635 t
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1920 1920	861 ccctttccttttaabaggccctgtggtctggggagaaatccctcagatcccactaaagtg 	B 8
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1800	7	å å
1740 1740	81 cgacaatgecetgetggeetgteteeetagggaatteetgetatgacagetggetageat 	g g
1680 1680	621 agacccagagccctctgagccgccact 	g dy
1620 1620		å Š
1560 1560	.501 acccagogotgotgogoatocaggacatacacocotttgotacgocotoat 	g dy
1500 1500	441 ttettgtteetgaagateatggetatgeteaecgageteegeageateaatgeteageae 	p 8
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1320 1320	1261 tacatgctgaagaagctgcagctgcatgaggaggagtatgtgctgatgcaggccatctcc	р ў
1260 1260	1201 ttggaagacactgcaggtggcttccagcaacttctactggagcccatgctgaaattccac	β δ
1200 1200	1141 ttcaacacagtgttcaacgcggagacttggaacctgggagtgtgggcggctgtcctactgc	В б
1140	081 cccatcgaggaccagatctccctgctgaagggggccgctttcgagctgtgtcaactgaga 	å 8
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RESULT 2
HSAJ9936
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HSAJ9936. 4448 bp mRNA PRI 08-SEP-1999 HOMO SAPIENS MRNA for nuclear hormone receptor PRR1. AJ009936. AJ009936.1 GI:5852062 nuclear hormone receptor; orphan nuclear receptor; PRR1 gene. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4448)

REFERENCE

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BASE COUNT
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Submitted (31-JUL-1998) Heard D.J., Novo Nordisk A/S, Molecular Genetics, Novo Alle, DK-2880, Bagsvaerd, DENMARK
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Identification of a novel protein isoform of the human nuclear hormone receptor PXR/SXR and localization to chromosome 3q12.1 - 13.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="truncated receptor"
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/db_xref="GI:5852063"
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 GGGAAAGAGATCTTCTCCCTGCTGCCCCACATGGCTGACATGTCAACCTACATGTTCAAA
            gggaaagagat:cttctccctgctgccccacatggctgacatgtcaacctacatgttcaaa 1035
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Qy 1815 aga Db 3376 AGA
Qy 1755 atg
Qy 1695 tgg Db 3256 TGG
Qy 1635 ctg Db 3196 CTG
Qy 1516 cgc Db 3076 CGC
Oy 1456 atc Db 3016 ATC
Oy 1396 ctg Db 2956 CTG
Qy 1336 cgc Db 2896 CGC
Qy 1276 ctg Db 2836 CTG
Qy 1216 ggt Db 2776 GGT
Oy 1156 aac Db 2716 AAC
Qy 1096 atc Db 2656 ATC
Qy 1036 ggc Db 2596 GGC

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JOURNAL MEDLINE FERENCE	LITLE	FERENCE	JRCE DRGANISM	EFINITION CESSION ERSION	-	4395	2834	4335	2774	4275	2714	4215	2654	15		9	534	035	2474	3975	2414	3916	2354	3856	2295	3796	2235	3736	2175	3676	2115
proc. Natl. Acad. Sci. U.S 98445350. 2 (bases 1 to 2802)	fileation of a human nuclear receptor defines a for CYP3A induction	<pre>per1a; Primates; Catarrhin1; Hominidae; 2802) 1802, Heidrich, J., Svensson, K., Asman, M., Je, Heidrich, J., Svensson, K., Blomquist,</pre>	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut	piens orphan nuclear receptor (PARZ) mkNA, compiete c 14.1 GI:3769536	AF084644 2802 bp mRNA PRI 20-OCT-1998	TACTTTTGG	gaattaaataatgtacttttggctaaaaaaaaaaaaaaa	TTGGGAAATGTAGCCCTGGGTTTAATGTCAAATCAAGG	acctaagaactagttttgggaaatgtagccctgggtttaatgtcaaaggc	CACTIGIGAÇIAAAAATTITTTIGCATTITICACAAAITATACTITATATAAGGCATTCCA 4334	acttgtgagtaaaaattttttttgcattttcacaaattatactttatataaggcattcc	TCTGTGTĄCACATCTATTCTCAAAGCTAAAGGGTATGAAAGTGCCTGCC	ctgtgtacacatctattctcaaagctaaagggtatgaaagtgcctgcc	N	rrtarartoaraatraattaaacacaccagagaagaaccatttacatgcaccttatat	15	cttgatggggcctgggtttgttcctggggctggaatgctgggtatgctctgtgac		ggcacaaactgcagctgtgagtgcgtgtgtgtgtgatttggtgtaggtag	TGTGATGGCCGGCACTGGGTACCCAAGTGAAGGTTCCCGAGGACATGAGTCTGTAGGAGC 4034	tgatggcaggcactgggtacccaagtgaaggttcccgaggacatgagtctgtaggag	AAGGAG-AAA,TGATAAGTGACAAAAGCAGCACAAGGAATTTCCCTTGTGTGGATGCTGAGC 3974	gagaaaatgataagtgacaaaagcagcacaaggaatttccctgtgtggatgctgag	TGGATC	tgagctcacagagtttatagtt-aaaaaaacaaacagaaacacaaacaatttg	TAAGCACCGATAATAGGTAGCCTGCTGGGGTATACAGCATTGACTCAGATATAGA	cactçataataggtagcctgctgtggggtatacagcattgactcagatatagat	TGGCATGACCTCATTCCGGCCACATCATTCTGTGTCTCTGCATCCATTTGAACACATT	gacctcattccggccacatcattctgtgtctctgcatccatttgaacacat	CTGTGGGAGTCCTCTAGAGAGAGAGAGGCCAGGAGGCCTGCACCAAATGTCAGAAG	tgtgggagt

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782 atttcaagaatttccggctgccaggggtgcttagcagtggctgcgagttgccagagtctc
                                                                                  722 ggatgatgatcagggagctgatggacgctcagatgaaaacctttgacactaccttctccc
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                                                            GGATGATGATCAGGGAGCTGATGGACGCTCAGATGAAAACCTTTGACACTACCTTCTCCC
                                                                                                                                          AGAAAAGTGAACGGACAGGGACTCAGCCACTGGGAGTGCAGGGGGCTGACAGAGGAGCAGC
                                                                                                                                                                                                                                                                                                        GGAAGACCCGGCGACAGTGCCAGGCCTGCCGCCTGCGCAAGTGCCTGGAGAGCGGCATGA 498
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/product="orphan nuclear receptor"
/product="114" *AAC64557.1"
/protein_id="AAC64557.1"
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/db_xref="01:3769537"
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RALIKKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTEDTTESHFKNERLDGVLS
SGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIF
SLLPHAADMSTYMFKGIISFAKVISYFRDLPIEDQISLLAKGAAFELCQLRFNYVFNAE
TGTWECGRLSYCLEDTAGGFQQLLLEPMLKHTYMLKKLQLHEEEYVLMQAISLFSPDR
PGVLQHRVVDQLQEQFAITLKSIIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL
LRIQDIHPFATPLMQELFGITGS"
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2 (bases 1 to
Heard,D.J.
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Submitted (31-JUL-1998) Heard
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 4337)
Heard,D.J., Holloway,J., Hansen,C., Tommerup,N.,
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Query Match 88.7%; Best Local Similarity 95.4%; Matches 2741; Conservative 1576 GAAATCATAACCTATGACTAGGACGGGAAGAGGAAGCACTGCCTTTACTTCAGTGGGAAT 1635 856 agggaagaagctgccaagtggagccaggtccggaaagatctgtgctctttgaaggtctct 915 gactttgtacactgtgaggacacagagtctgttcctggaaagcccagtgtcaacgcagat 375 ACCGGATTGTTCAAAGTGGACCCCAGGGGAGAAGTCGGAGCAAAGAACTTACCACCAAAC 1815 gaatcgatagtgaattcgtgggacgggaagagggaagcactgcctttacttcagtgggaat 75 CAGTGCCAGGCCTGCCGCCAAGTGCCTGGAGAGCGGCATGAAGAATGAGATGATC gcccggctgaggtgccctttccggaagggcgcctgcgagatcacccggaagacccggcga ttcaatgtcatgacatgtgaaggatgcaagggctttttcaggagggccatgaaacgcaac GACTITGTACACTGTGAGGACACAGAGTCTGTTCCTGGAAAGCCCCAGTGTCAACGCAGAT 1935 accggattgttcaaagtggaccccaggggagaagtcggagcaaagaacttaccaccaagc gagctgatggacgctcagatgaaaacctttgacactaccttctccccatttcaagaatttc 795 atgtccgacgaggccgtggaggagaggcggggccttgatcaagcgggaagaaaagtgaacgg acagggactcagccactgggagtgcagggggctgacagaggagcagcggatgatgatcagg 735 cagtgccaggcctgccgcctgcgcaagtgcctggagagcggcatgaagaaggagatgatc cggctgccaggggtgcttagcagtggctgcgagttgccagagtctctgcaggccccatcg 855 ATGTCCGACGAGGCCGTGGAGGAGAGGCGGGCCTTGATCAAGCGGAAGAAAAGTGAACGG ACAGGGACTCAGCCACTGGGAGTGCAGGGGGCTGACAGAGGAGCAGCGGATGATGATCAGG 1134 a RKCLESGMKNEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA QMKTEDTTESHEKNERVSLQLAGEDGSVWNYKEPADSGGKEIFSLLEHHADMSTYMEK GIISFAKVISYERDLE IEDQISLLKGAAFELGQLEFNTYPHAETGTWEGGELSYCLED TAGGFQQLLLEPMLKFHYMLKKLQLHEESTYLMQAISLESPDREGVLQHRVVDQLQEQ FAITLESYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQ 1105 c score 2575.6; Pred. No. 0; O; Mismatches 1056 g 1042 t DB 52; 19; Indels 114; Gaps Length 4337; 1995 2175 2115 2055 1875 2357 2355 2295 2235 675 615 555 495 435 255 4.

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                                                                                                                                                                                                                 Submitted (21-APR-1998) Molecular Moore Drive, RTP, NC 27709, USA Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 0;
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                                          cycatccaygacatacacccctttyctacycccctcatycaygayttyttcyycatcaca 1575
                                                                                                                                                                                       cgcccaggtgtgctgcagcaccgcgtggtggaccagctgcaggagcaattcgccattact 1395
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          ggtagctgagcggctgcccttgggtgacacctccgagaggcagccagacccagagccctc 1635
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GGTAGCTGAGCGGCTGCCCTTGGGTGACACCTCCGAGAGGCCAGACCCAGAGCCCTC
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                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 160185)

RS MuznyD.M., Adams.C., Bailey.M., Barbaria,J., Blankenburg.R.,
Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay.C., Bunac.C.,
Burkett,C., Burrows,J., Carter.M., Chacko,J., Chen,Z., Cox,C.,
Burdar,C., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,J.L.,
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
Holloway.C., Hosak,H., Jackson,L.E., Jackson,A., Hogues,M.,
Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J.,
Lucler,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,
Morris,S., Nash,S., Nelson,A., Nguyen,N., Nguyen,S.,
Oswal,G., Nash,S., Nath,S., Nath,S., Payton,B., Perez,L., Pu,L.L.,
Oswal,G., Partsh,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R.,
Tabor,P., Taylor,T., Vasquez,L., Vilson,R., VO,O., Wabbah,M.,
Warllagton,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGTGCCCCCACCCCCAGTTCAGTCTGTAGGGAGTGAAGCCACAGACTCTTACGTGGA 1839
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Homo sapiens chromosome 3 clon
SEQUENCE, 34 unordered pieces.
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AC069444.7 GI:9719625
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  Worley, K.C.
                                      Unpublished
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3 clone RP11-169N13, WORKING DRAFT
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On Aug 7, 2000 this sequence version replaced g1:8699996.
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Submitted (30-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence, It currently consists of 34 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-primer Bodipy: 6% of reads
Chemistry: Dye-terminator Big Dye: 94% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 132114 bases at least Q40
Consensus quality: 142928 bases at least Q20
Consensus quality: 147607 bases at least Q20
Consensus quality: 147607 bases at least Q20
Estimated insert size: 148422; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sgarose-fp estimation
Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
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Center project name: HMTO
Center clone name: RP11-169N13
Center Summary Statistics
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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88644: gap of
88644: gap of
91971: contig
92071: gap of
98127: contig
98227: gap of
104128: contig
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Best Local Similarity 98.4%;
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                                 TGTAGGGAGTGAAGCCCACAGACTCTTACGTGGAGAGTGCACTGACCTGTAGGTCAGGACC
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/db_xref="taxon:9606"
/chromosome="3"
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MEDLINE
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                                                                                                                                                                        356 agcccagtgtcaacgcagatgaggaagtcggaggtcccccaaatctgccgtgtatgtgggg 415
                                                                                    207 AAGGCAGTGGGAAACAAGCTGGCCTTGCGCGCTGTGATGAAGCAGACTCCATGGGTGGAA 266
                                                                                                           296 aagaaagctgyaaccatyctgactttgtacactgtgaggacacagagtctgttcctggaa 355
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AF182217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus pregnane x receptor (NR112) mRNA, complete
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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TVKRNAKLRCPFRKGACEITRKTRRCCQACRLEKCLESGMKEMIMSDYAVAQRRALI
KRKKREMEAQPPGMQGLTGEQRMIIEELMDAMKTFDTTFSHFKNFRLPEFULGSGE
KRKKREMEAQPPGMQGLTGEQRMIIEELMKLSLQLEGEGSVWNYTPPADRSGKKLFSLLP
HLADMSTYMFKGIINFAKVISYFRDLFIEDQISLLKGATLELCLLRFNTVFNAETGTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="NR112"
/note="PXR; nuclear receptor subfamily 1 group I member 2;
zinc-finger protein; transcription factor"
/codon_start-1
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DTHPFATPLMRELFSTTDD"
3556 c 535 g 370 t
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/protein_id="AAD54426.1"
/db_xref="GI:5853354"
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/strain="breed New Zealand white rabbit"
/db_xref="taxon:9986"
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/note="PXR"
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Pred. No. 3e-216;
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Query Match Best Local

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An orphan nuclear receptor activated by pregnanes defines a novel steroid signaling pathway (2019) 73-82 (1998)
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Submitted (29-OCT-1997) Department of Molecular Endocrinology, Glaxo Wellcome, 5 Moore Drive, RTP, NC 27709, USA
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Jones,S.A., McKee,D.D., Oliver,B.B., Willson,T.M.,
Zetterstrom,R.H., Perlmann,T. and Lehmann,J.M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Direct Submission
Submitted (20-SEP-1999) Molecular
Submitted (70-SEP-1999) Molecular
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1. (bases 1 to 1601)
Jones, S. A., Moore, L.B., Shenk, J.L., Wisely, G.B., Hamilton, G.A., McKee, D.D., Tomkinson, N.C., LeCluyse, E.L., Lambert, M.H., Wilson, T.M., Kilewer, S. A. and Moore, J.T.
Wilson, T.M., Kilewer, S. A. and Moore, J.T.
The pregnane X receptor: a promiscuous xenobiotic receptor that he diverged during evolution
Mol. Endocrinol. 14 (1), 27-39 (2000)
                                                                                                            Jones, S.A., Moore, L.B., Shenk, J.L., Wisely, G.B., Ha
McKee, D.D., Tomkinson, N.C., LeCluyse, E.L., Lambert,
Willson, T.M., Kliewer, S.A. and Moore, J.T.
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                                          TGACATGTCAACCTACATGTTCAAAGGCATCATCTACTTTGCTAAAGTCATCTCCTACTT 722
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                                                                                                                                                                                                                                                                                                                                                                  G36929.1
STS.
                                           Email: myers@shgc.stanford.edu
primer A: CCCATCAAGTGGCAAACAGA
Primer B: AGTGAAGGTTCCCGAGGACA
STS size: 107
PCR Profile:
                                                                                                                                                       Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
                                                                                                                         Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 365)
                                                                                                                                                                                                                                                                                                                                                                                                                               G36929
                                                                                                                                                                                                      Contact: Richard M. Myers
                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                  G36929
                                                                                                                                                                                                                                                                                                                                                                                                               SHGC-56597 Human Homo
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                               Initial incubation: 95 degrees C for 10
Denaturation:
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                                  AF276753 1340 bp m
Gallus gallus xenobiotic
AF276753
AF276753.1 GI:10505178
chicken.
Gallus gallus
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Pred. No. 9.4e-59;
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AUTHORS
TITLE
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TITLE
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PUBMED
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Best Local Similarity 57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 676;
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                                                                                                                 tyaacygacagygactcayccactyyyaytycayyyyctyacayayyaycaycgyatyat 728
                                                                                                                                                                                                             gatgatcatgtccgacgaggccgtggaggagaggcgggccttgatcaagcggaagaaaag
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CATCAGCATCCTCATCGCCGCGCACAAACGCACCTTCGACTCCAGCTTCTCCCAGTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-JUN-2000) Division of Pharmacology/Neurobiology, Biozentrum of the University of Basel, Klingelbergstrasse 70, 4056, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1340)
Handschin,C., Podvinec,M. and Meyer,U.A.
CXR, a chicken xenoblotic-sensing orphan nuclear receptor, related to both mammallan pregnane X receptor (PXR) and constitutive androstane receptor (CAR)
PIOC. Netl. Acad. Sci. U.S.A. 97 (20), 10769-10774 (2000)
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Handschin, C. and Meyer, U.A.
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/product="xa618374.1"

/db_xref="G1:10505179"

/db_xref="G1:10505179"

/translation="MSQSSPSDPDSPGAORCPNVTDVTEELKVCAVCGDRATGYHFH
/MSCEGCKGFFRRSILKGVHFTCPFTRSCPITKAKRROCQACRLACKCLDVGMRKDMIN
SEEALGBRRALRLORRLAQAOPGGLTAEOGGLISILISILISHKRTFDSSFSOFOHYOPAN
RLCIPGPCSQSPFGFGVPSASLSFQLDCLDEDVLPDVFSILPHFADLSTFMIQOYIKF
RKEIPAPRGLPIDDQISLKKARATIGICQIQFNTVFNEETNAWECGQHCFTIKDGALAG
FQQIYLEPLKKFHISLKKLRLHEAEYVLLVAMLLFSPDHASVTGDFIDGLGEKVALT
LKSYIDHRHMPEGGFIYAKLLLLILTELGTLKWENTRQILHIQDLSSWTPLLSEIIS"

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/note="xenobiotic-sensing orphan nuclear receptor"
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/db_xref="taxon:9031"
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1. .1340
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Pred. No. 3e-48;
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                                                                                       GGGGGGCTGACAGCAGAGCAGCAGGAGCT
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                                 Submitted (29-JUN-1994) to the DDBJ/EMBL/GenBank databases. Yasutomi Kamel, Kyoto University, Food Science and Technology; Kitashirakawaolwake-cho, Sakyo-ku, Kyoto, Kyoto 606-01, Japan (Tel:075-753-6263, Fax:075-753-6264)
                                                                                                                                                                                                             vitamin D receptor; VDR.
Mus musculus cell_line:3T3-L1 cDNA to mRNA, clone_lib:lambda ZAP
Kamei,Y.,
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 Fukuwatari,T.,
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 Ono, T.,
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 Kato, S. and Sugimoto,
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TCCACGATGGATCTGAATGAAGAAGGCTCCGATGACCCCTCTGTGACCCTGGACCTGTCT
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/KGFFRRSMKRKALFTCPFNGDCRITKDNRRHCQACRLKRCVDIGMKEEILTDEEVQR
KREMIMKRKEEBALKUSLRPKLSESQOHIAILLDAHHKTYDFTYADFREDFIPFNAD
VSTGSYSFRPTLSFSGDSSSNSDLYTPSLDMMEPASFSTMDLNEEGSDDPSVTLDLSP
LSMLPHLADLYSTSIOKVIGFAKMIPGFRDLTSDDQTVLLKSSALTEVIMLRSNQSFTM
DDMSWDCGSQDYKYDITDVSRAGHTLELIEPLIKFQVGLKKLNKLHEEBHYLLMAICIV
SDDRFGVQDAKLVEAIQDRLSWTLQTYIACRHPPPGSHQLYAKMIQKLADLRSLNEEH
SKQYRSJSFQPENSMKLTPLVLEVFGNEIS"
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/protein_id="BAA06737.1"
/db_xref="GI:699619"
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109. .1377
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/db_xref="taxon:10090"
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J04147 J03630
J04147.1 GI:2
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Burmester, J.K., Wiese, R.J., Maeda, N. and DeLuca, H.F.
Structure and regulation of the rat 1,25-dihydroxyvitamin
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Burmester, J.K., Maeda, N. and DeLuca, H.F.
Isolation and expression of rat 1,25-dihydroxyvitamin
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Rat (Sprague-Dawley) kidney and intestine, cDNA to mRNA.
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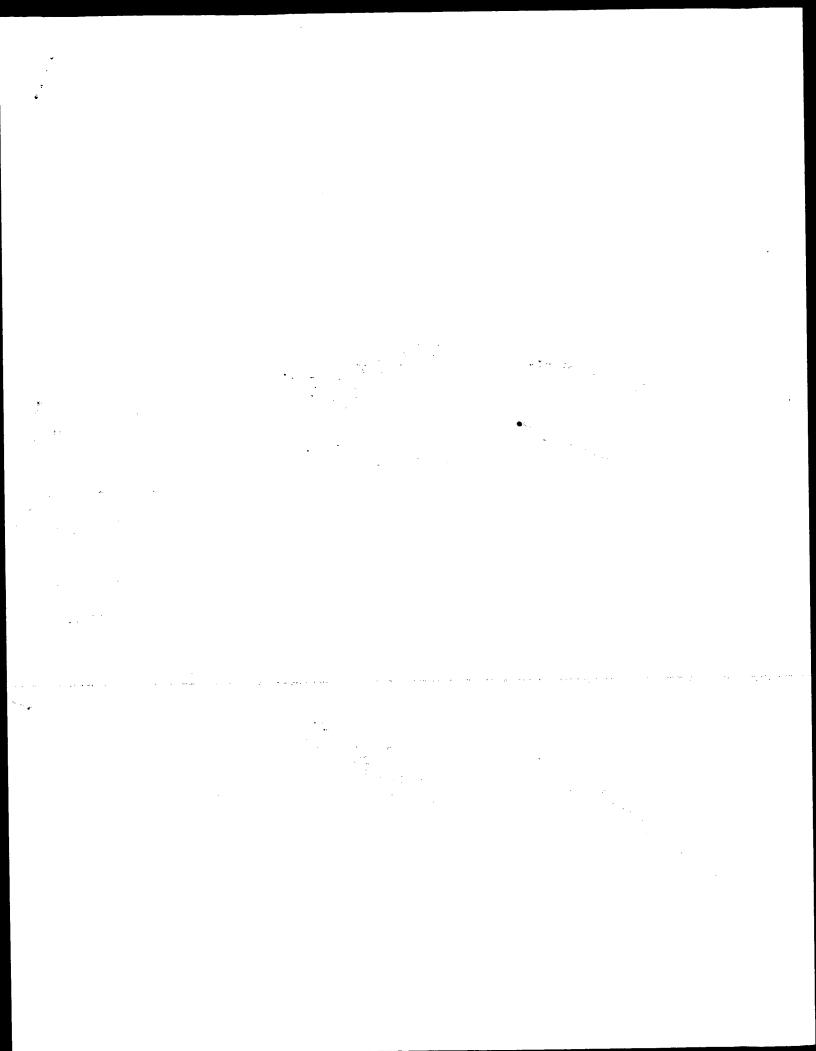
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Direct Submission
Submitted (30-JUN-1997) Biochemistry, University of
Submitted (30-JUN-1997) Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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AF011356
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Cloning and origin of the two forms of chicken vitamin
Arch. Biochem. Biophys. 339 (1), 99-106 (1997)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Q9unw4 homo Q9uj27 homo Q9uj28 homo Q9uj28 homo Q9uj23 homo Q9uj23 homo Q9uj23 homo Q9uj23 homo Q9uj27 rat Q9r187 rat Q9uj83 yen Q9ib73 par Q9pr18 bra Q9ib74 par Q9gus1 rat Q9qus1 rat Q9qus7 mus Q12970 homo Q92943 homo Q76246 uca Q9pve4 bra	Description
9unw4 homo sapien 9uj26 homo sapien 9uj26 homo sapien 9uj24 homo sapien 9uj23 homo sapien 9uj23 homo sapien 9uj25 homo sapien 9uj27 rattus norv 9uj22 homo sapien 9uj22 homo sapien 091839 xenopus lae 091b73 paralichthy 09prn2 brachydanio 09pr4 paralichthy 09pr3 rattus norv 109us1 rattus norv 109us1 rattus norv 109us1 ratus norv	ion
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PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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          Receptor.
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                                                                                                                                Hum.
                                                                       ; IPR000324; -.; IPR000536; -.; IPR001628; -.; IPR001723; -.
 434
                                                                                                                                                                                                                                                               (TrembLrel. 13, Created)
(TrembLrel. 13, Last sequence update)
(TrembLrel. 15, Last annotation update)
                                                                                                                               Genet.
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                  PXR,
                                                                                                                                         West and
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                                                                                                                                                                                                                       Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                       PRT;
AB36DEC23C4C4200
                                                                                                                                                                          Tommerup N.,
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i; Hominidae; Homo.
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CRC64;
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Query Match

99

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SOUR BEAR AND DESCRIPTION OF THE SOURCE SOUR
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                                                        INTERPRO; IPRO01628; ...
INTERPRO; IPRO01723; ...
PRAM; PF00104; hormone_rec; 1.
PFAM; PF00105; rf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                    EMBL; AJ009936; CAB55
HSSP; P10826; 1HRA.
INTERPRO; IPR000324;
INTERPRO; IPR000536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
01-MAY-2000
01-OCT-2000
Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UJ26;
                                                                                                                                                                                                                                                                                      Eur. J. Hum. Genet.
                                                                                                                                                                                                                                                                                                                                                                   Heard D.J., Holloway Vissing H.;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                   PROSITE; PS00031;
                                                                                                                                                                                                                                                                                                      hormone receptor PXR/
-13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                              'Identification of a novel
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  457
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(TIEMBLIel. 13, Last sequence up
(TIEMBLIEL. 15, Last annotation
MONE RECEPTOR PRR1-C.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                           localization
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Best Local Sim
Matches 431;
INTERPRO: IPRO01628; -.
INTERPRO: IPRO01728; -.
INTERPRO: IPRO01728; -.
INTERPRO: IPRO01728; -.
PEAM; PF00104; hormone_rec; 1.
PEAM; PF00105; zf-C4; 1.
PRINTS; PR00347; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00546; THYROIDHORMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UJ24 PRELIMINARY; PRT; 397 AA. 09UJ24; O1-MAY-2000 (TrEMBLrel. 13, Created) O1-MAY-2000 (TrEMBLrel. 13, Last sequence up O1-OCT-2000 (TrEMBLrel. 15, Last annotation
                                                                                                                                                                                                                                  HSSP;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                             ISSUE-LIVER;
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AJ009937;
P10826; 1H
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                                                                                                                                                                                                                                                                                                                                                  D.J., Holloway J., Hansen C., ng H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVDQLQEQFAITLKSYIECNRPQPAHRELELKIMAMLTELRSINAQHTQRLLRIQDIHPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCELPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLL
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                                                                                                                                                                                                            IPR000324;
                                                                                                                                                                                                                                           Genet. 0:0-0(0)
37; CAB5 492.1;
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                                                                                                                                                                                                                                  1HRA
                                                                                                                                                                                                                                                                                                                                 of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                 novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.5%;
99.3%;
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Pred. No. 3.8e-184;
1; M1smatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                             isoform
                                                                                                                                                                                                                                                                                                                                                                   Tommerup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi; i; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                   of the human nuclear
to chromosome 3q12.1
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                                                                                                                                                                                                                                                                                                                                                                   Aagaard
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Best Local S
Matches 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UJ23
Q9UJ23;
Q1-MAY-2000
Q1-MAY-2000
Q1-CCT-2000
                                       INTERPRO;
INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                        PRR2.
PRR2.
Homo sapiens (Human).
Homo sapiens (Human).
harvota; Metazoa; Chordata;
haria; Primates;
                                                                                                       INTERPRO; INTERPRO;
                                                                                                                                                                                                            hormone receptor PXR/SXR and -13.3.";
                                                                                                                                                                                                                                                                               Heard D.J.,
Vissing H.;
                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE 397 AA; 45782 MW; 5E2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324
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                                                                                                                                              J. Hum. Genet 0:0-0(0)
AJ009937; CAB55493.1;
P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPLMQELFGITGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VSLQLRGEDGSVWNYKPPADSGGKEIFSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HORMONE
                                    IPRO00324; -...; IPRO00536; -...; IPRO01628; -...; IPRO01723; -...; IPRO01728; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 15, Last annotation updat
MONE RECEPTOR PRR2-C.
                                                                                                                                                                                                                                                                                                   Holloway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                 J., Hansen C.,
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                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Ve Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                               Tommerup N., Aagaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                              of the human nuclear to chromosome 3q12.1
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Best Local S
Matches 394
                                                                                                                                                                                                                                                                                                                                                                                                           Q9UJ25

Q9UJ25;
Q9UJ25;
Q1-MAY-2000 (TIEMBLIEL. 13, Created)
Q1-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
Q1-CT-2000 (TIEMBLIEL. 15, Last annotation updat)
Q1-CT-2000 (TIEMBLIEL. 15, Last annotation updat)
EMBL; AJ009936; CAB55491.
HSSP; P10826; 1HRA.
INTERPRO; IPR000324; -.
INTERPRO; IPR000536; -.
INTERPRO; IPR001628; -.
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SEQUENCE
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PRINTS; PRO0350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00546; THYROIDHORMR.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                            Heard D.J., Holloway
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                               Eur. J.
                                                                                                                                  hormone receptor PXR/SXR and localization -13.3.";
                                                                                                                                                                                                                                                    TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
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                                                                                                                                                                                  'Identification
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Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                chromosome
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3q12.1
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PRAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-20092336; PubMed=10628745;

JONES S.A., MOOTE L.B., Shenk J.L., Wisely

MCKee D.D., Tomkinson N.C., LeCluyse E.L.,

Kilewer S.A., Moore J.T.;

"The pregnane X. receptor: a promiscuous xe

diverged during:evolution.";

MOI. Endocrinol. 14:27-39(2000).

EMBL; AF182217: AAD54426.1; -.

EMBL; AF188476; AAF31165.1; -.
                                                                                                                                                                                                                            01-MAY-2000 (TIEMBLIEL 13, Created)
01-MAY-2000 (TIEMBLIEL 13, Last seq
01-OCT-2000 (TIEMBLIEL 15, Last ann
PREGNAME X RECEPTOR.
NR112 OR PXR.
                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                 Q9TU02;
                                                                                                                   STRAIN-BREED NEW ZEALAND WHITE RABBIT; TISSUE-KIDNEY; Savas U., Wester M.R., Griffin K.J., Johnson E.F.; "The rabbit pregnane x receptor is activated by rifampicin."; submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             Q9TU02
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=9986;
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Local Similarity
hes 378; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIHPFATPLMQELFGITGS 434
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                                                                                                                                                                                                                                                                                             PRELIMINARY;
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99.7%;
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Pred. No. 1.6e-158;
                                                                                                                                                                                                                                                                                               PRT;
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                                                                  Wisely
se E.L.,
                                                                                                                                                                                                                                                                                                411
                                              xenobiotic
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                                                                  G.B., Hamilton Lambert M.H., W
                                                                                                                                                                                                                                                    update)
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                                                                    Willson T.M.,
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                                                that has
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Best Local Similarity
Matches 339; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    Q9R1A7;
01-MAY-2000 (TrEMBLrel. 13, C;
01-MAY-2000 (TrEMBLrel. 13, L;
01-OCT-2000 (TrEMBLrel. 15, L;
PREGNANE X RECEPTOR.
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INTERPRO; IPR000324; -.
INTERPRO; IPR000358; -.
INTERPRO; IPR0001628; -.
INTERPRO; IPR001628; -.
INTERPRO; IPR001723; -.
PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PFAM; PF001047; STROIDFINGER.
PRINTS; PR00380; VITAMINDR.
PRINTS; PR00380; VITAMINDR.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1
  STRAIN-SPRAGUE-DAWLEY;
Shang H., LeCulyse E., Liu L., Hu M., Matoney L., Zhu W., Yan B.;
Zhang H., LeCulyse E., Liu L., Hu M., Matoney L., Zhu W., Yan B.;
Wat Pregnane X Receptor: Molecular Cloning, Tissue Distribution,
Xenobiotic Regulation.";
Arch. Biochem. Biophys. 368:14-22(1999).
Arch. Biochem. Biophys. 368:14-22(1999).
EMBL; AF151377; AAD47214.1; -.
HSSP; P10826; 1HRA.
INTERPRO; IPR000324; -.
INTERPRO; IPR001628; -.
INTERPRO; IPR001628; -.
INTERPRO; IPR001723; -.
                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9R1A7
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                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
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llarity 83.1%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
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Pred. No. 4.2e-145;
4; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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       Q907022
ID Q90
AC Q99
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Best Local Similarity
Matches 330; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UJ22
Q9UJ22;
Q1-MAY-2000
01-MAY-2000
01-OCT-2000
EMPI; J. Hum. Genet. 0:0-0(0).

EMBI; AJ009937; CAB55494.1; -.

HSSP; P10826; 1HRA.

INTERPRO; IPR000324; -.

INTERPRO; IPR000536; -.
                                                                                                                                                                                                                                                                                                                                    hormone receptor -13.3.";
                                                                                                                                                                                                      Heard D.J., Holloway J.,
Vissing H.;
                                                                                                                                                                                                                                                         TISSUE-LIVER;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                          "Identification of a novel pu
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(Tremblrel. 13, Last sequence update)
(Tremblrel. 15, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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302 239 242 179 182

299

Hansen protein

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Tommerup N.,

Aagaard

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

localization

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of the human nuclear to chromosome 3q12.1

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PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1
PRINTS; PR00047; STROIDEINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1
Receptor.
Receptor.
SEQUENCE 431 AA; 49660 MW; 48545F
                                                                                                                                                                                                                 GFFRRAMKRNVRLRCPFRKGTCEITRKTRROCQACRLRKCLESGMKKEMIMSDAAVEORR
                                                                                                                                                                                                                                                                                                                                                                                                                                  DQLQEQEAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFAT
                                                                                                                                                                MADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECG
                                                                                                                                                                                                                                                                                                                                                                                GFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERR
                                                                     RLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVV
                                                                                                                                            LADVSTYMFKGVINFAKVISHFRELPIEDQISLLKGATFEMCILRFNTMFDTETGTWECG
DQLQERFALTLKAYIECSRPYPAHRFLFLKIMAVLTELRSINAQQTQQLLRIQDTHPFAT
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76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1761.5;
Pred. No. 1.3e
12; Mismatches
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les 57;
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DT DT Q9
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Best Loc
Matches
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PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00346; THYROIDHORMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91839;
Q91839;
Q1-NOV-1996;
Q1-NOV-1996;
Q1-MAY-2000;
                                                                                         SEQUENCE FROM N.A.

MEDLINE-94173664; PubMed-8127656;

Smith D.P., Mason C.S., Jones E.A., Old R.W.;

Smith D.P., Mason C.S., Jones E.A., old R.W.;

A novel nuclear receptor superfamily member in Xenopus that associates with RXR, and shares extensive sequence similarity mammallan vitamin D3 receptor.";

Nucleic Acids Res. 22:66-71(1994).

EMBL; X75165; CAA53006.1; -.

HSSP; P10826; LHRA.
                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 13, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
0RPHAN NUCLEAR RECEPTOR OF STEROID/THYROID SUPERFAMILY.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eut.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pij
     PFAM;
                                                   INTERPRO; IPR000536; -. INTERPRO; IPR001628; -.
                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
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SEQUENCE
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIHPFATPLMQELFGITGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKE
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       PF00104;
PF00105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIHPFATPLMQELFGITGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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     hormone_rec;
zf-C4; 1.
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Pred. No. 4.7e-140;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386
                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
ia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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                                              Query Match
Best Local S
Matches 179
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Best Local
                                                                                                                                                                                                                                                                                                                                 Q9IB73
Q9IB73;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2000
                                                                                                           Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                          VITAMIN D
VDRA.
                                                                                                                                 Suzuki T., Suzuki N., Srivastava A.S., Kurokawa "Identification of cDNAs encoding two subtypes of in flounder, Paralichthys olivaceus."; Biochem. Biophys. Res. Commun. 270:40-45(2000). EMBL, AB037674; BAA95016.1; -.
                                                                                                                                                                                                                                Paralichthys olivaceus (Flounder).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rotinopterygii; Nelostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Bothidae; Paralichthys.
NCBI_TaxID-8255;
                                                                                                                                                                                    Suzuki T., Suzuki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS: PRO0047: STROIDFINGER.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
SEQUENCE 386 AA; 44302 MW; 8B046
                                                                                                                                                                                               TISSUE-INTESTINE;
                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 328
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hes 179;
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            VNADE-EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEIT
 VGPDEFDRNAFRICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKASFTCPF-NGSCTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIECNR-PQPAHRELFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FIDSQRPPSPQNRLLYPKIMECLTELRTVNDIHSKQLLEIWDIQPDATPLMREVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT-AGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLGVQGLTEEQRAMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQLFLEPLVRIHRMMRKLNLQSEEYAMMAALSIFASDRPGVCDWEKIQKLQEHIALTLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAKMLPYFKSLDIEDQIALLKGSVAEVSVIRFNTVFNSDTNTWECGPFTYDTEDMFLAGF
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                                             Similarity 43.179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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000 (TrEMBLIEL 15, 1
000 (TrEMBLIEL 15, 1
D RECEPTOR A.
                                                                                                           420
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                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                           ŘΑ;
                                                                                                           47486 MW;
                                                           35.7%;
43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSSDPT---QEPQATS--SEAFLMLPHISDLVTYMIKGIIS
                                               70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                              Score 817; DB 13;
Pred. No. 6.3e-61;
70; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 991.5; I
Pred. No. 1.1e:
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                           038FBF00D4F38067
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                                                                                                                                                                       T.;
of vitamin
                                                                                                           CRC64
                                                                     Length
                                               Indels
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Best Local :
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01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Danid rerio vitamin D receptor.";
submitted (JUL-1999) to the EMBL/G
EMBL; AF166512; AAF21427.1; -.
HSSP: P20393; 1A6Y:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPRO00324; -.
INTERPRO; IPRO00536; -.
INTERPRO; IPRO01628; -.
INTERPRO; IPRO01723; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PTN2
               127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244
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                                                                                                             RAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIK 126
RKKSE---RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSS
                                                      RSMKRKASFTCPF-NGNCTITKDNRRHCQACRLKRCIDIGMMKEFILTDEEVQRKKDLIM 140
                                                                                                                                                                      ESTVNGDATSLMDLMAVSTSATGQDQFDRNAPPICGVCGDKATGFHFNAMTCEGCKGFFR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGFRDLTAEDQIALLKSSAIEIIMLRSNQSFSLEDMSWSCGGPDFKYCINDVTKAGHTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00104; hormone_rec; 1.
PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECG--RLSYCLED-TAGGFQQL
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                                                                                                                                                                                                                                                                                                      178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLEPLVKFQVGLKKLNLHEEEHVLLMGICLLSPDRPGVQDHARVEQLQDRLPEALQAYIR 363
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                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           453 AA; 50765 MW;
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        34.6%; Score 792; DB 13; 40.3%; Pred. No. 8.9e-59;
                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           B52C82C185859F9C CRC64;
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                                                                                                                                                                                                                                                                                            158;
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                                                                                                                                                                                                                                                                                         Gaps,
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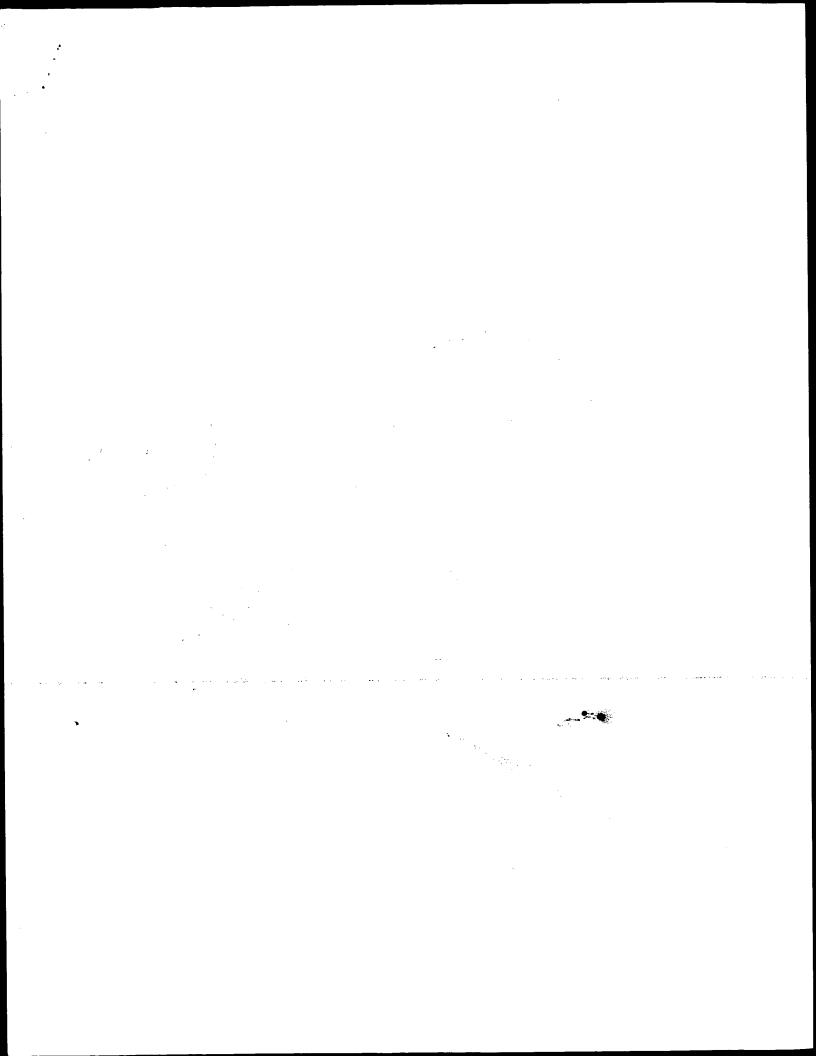
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Best Local;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki T., Suzuki N., Srivastava A.S., Kurokawa "Identification of cDNAs encoding two subtypes o in flounder, Paralichthys olivaceus."; Blochem. Blophys. Res. Commun. 270:40-45(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Bothidae; Paralichthys.
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VITAMIN D RECEPTOR B.
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                                     247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paralichthys olivaceus (Flounder).
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                                                                                                                                                                                                                                       134 GTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSSGCELPESLQA 190
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                                                                                                                                                                                                                                                                                                   63 NGSCTITKDNRRHCQACRLKRCVDIGMMREFILTDEEVQRKKDLIQRRKDEEAQREAERE
                                                                                                                                                                                                                                                                                                                                                      81 KGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKK-----SERT 133
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                                                                                                                                   PSREEAAKWSQVRKDLCSLKVS----LQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADM 246
                                                                                                                                                                                         ARRP----RLTDEQSQVIAMLVEAHKTYDDSYSDFCRFRPPVREGPVTRSASRAASLHS
                                                                                  LSDASSDSFSHSPESV-DTKVNFNNLLMMYQEQGS----SPDSSEEEGSSFSMLPHLADL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.5%; Score 790.5; DB: 41.6%; Pred. No. 1.1e-58
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PFAM; PF00105; zf-C4; 1.
PRAM; PF00047; STGIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00546; THYROIDHORME.
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01-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sexually dimorphic nuclear translocation of receptor CAR and induction of CYP2B1 gene by phenobarbital in rat livers."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AP133095; AAF22567.1; -. EMBL; AP133094; AAF22566.1; -. EMBL; P19793; ZNLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
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INTERPRO; IPR001628; -.
INTERPRO; IPR001723; -.
INTERPRO; IPR001728; -.
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                                                                                                                                                                                                                                                                                                                 TLLGAHTRHVGPMFDQFVQFRPPAYLFSH-HRPFQPLAP-----
                                                                                                                                                                                                        HCPACKLQKCLNVGMRKDMILSAEALALKRARQAKRRAQKASLQ-----LSQQQKELIQ 125
                                                LQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQ 272
                                                                                                                                                       ELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVS
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 729; DB 11;
; Pred. No. 1.4e-53;
61; Mismatches 122
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Last sequence update)
Last annotation updat
     -VLPLLTHFADINTFMVQQIIKFTKDLPLFRSLTMEDQ
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Best Local
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Albert1 S., Steffensen K.R., Gustafsson J.A.;
Albert1 S., Steffensen K.R., Gustafsson J.A.;
Cloning and characterisation of nuclear oxyster and LXRb from mouse.";
brear:
and LXRb from mouse.";
characterisation of nuclear oxyster and LXRb from mouse.";
characterisation of nuclear oxyster and LXRb from mouse.";
characterisation of nuclear oxyster and LXRb from LXRb
                                                                                                                                                                                        Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00546; THYROIDHORMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9QUH7;
Q9QUH7;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TIEMBLIE1. 13, Created)
01-MAY-2000 (TIEMBLIE1. 13, Last sequence update)
01-OCT-2000 (TIEMBLIE1. 15, Last annotation update)
NUCLEAR OXYSTEROL RECEPTOR LXR-ALPHA (LXR-ALPHA).
NR1H3 OR LXR-ALPHA.
                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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133 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAQATS 189
                                                78
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                                                                                                                                  18 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 77
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                                           PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 131
                                                                                            EPTELRPOKRKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGARYVC 132
                                                                                                                                                                                                                                                                                                                                                PS00031;
                                                                                                                                                                                                             Similarity
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Pred. No. 1.
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                                                                                                                                                                                            142;
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424 LMQELFGI 431
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436 LLSEIWDV 443
                        307 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSDDRPGYLQHRVVDQL 365
                                                                             229 --- DRLRVTPW-PIAPD------ 260
                                                                                                                     189 QAPSREEAAKWSQYRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 248
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Search completed: February 18, 2001, 13:05:04 Job time: 6193 sec



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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. /cgn2_2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2. /cgn2_2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3. /cgn2_2/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4. /cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5. /cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5. /cgn2_2/gcgdata/geneseq/geneseqp/AA1985.DAT:*
6. /cgn2_2/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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Gapop 10.0 , Gapext 0.5
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2290
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               cgn2_2/gcgdata/geneseq/geneseqp/An198.DAT:

cgn2_2/gcgdata/geneseq/geneseqp/An198.DAT:

cgn2_2/gcgdata/geneseq/geneseqp/An198.DAT:

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cgn2_2/gcgdata/geneseq/geneseqp/AA2000.DAT:*
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231.913 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

12	110	ဖထ	70	ហ	4	w	ພ	مو	Result No.
1585	2169 2165	2287 2287	2287	2287	2287	2287	2287	2296	score
69.2	94.7 94.5	99.9 99.9	99.9	99.9	99.9	99.9		100.0	Match bength
316	434 414	473 473	4/3	466	457	457	434	437	
20	220	20	20	20	20	20	20	20	DB B
Y42689	Y21799 Y42691	Y15933 Y09516	X15936	Y25410	Y15932	Y16035	Y15931	Y09515	ID
His6-pregnane X re	Human steroid and Human pregnane X r	A human intranucle Human vitamin D re	A human intranucle	Human nNR7 partial	A human intranucle	A human intranucle	A human intranucle	Human vitamin D re	Description

Ligand binding dom	Y21631	20	ത	19.4	445	Ğ
(O)	P80921		ιn		448	4
Retinoid X recepto	R99735	17	484		451.5	ω
Farnesoid-activate	W03448	17	C)		454	2
1010	W40072	19	~		C)	Ħ
. Homo sapi	R33744	14	۵		481.5	5
ubiquitous	W25035	18	443		483	9
Rat ubiquitous nuc	R74739	16	443		483	ĕ
OR-1 orphan recept	R94169	17	446		487	7
	R99736	17	446		490	6
LXR-alpha, orphan	W03326	17	447	21.5	491.5	ភ
foeta	R96234	17	461		495	4
Human ubiquitous n	W25034	18	460		496	ũ
æ	R98140	17	461		498	ະ
	R97982	17	461		498	ä
Human recombinant	R52980	15	461	21.7	498	õ
ubiquitous	R74738	16	460		498	õ
se CNREB-1.	Y32374	21	445	•	498.5	8
vitamin D	R43656	14	367	•	632	7
vitamin D	W94622	20	356	٠	656	õ
-	W37261	19	356	•	656	Ğ
CAR	W93903	20	358	٠	725	ž
nucl	Y17872	20	357	•	733.5	ພັ
CAR	R41346	14	348	•	763	_ເ
CAR recepto	W93902	20	348	•	768	ï
itutively ac	W32536	18	348	•	768	õ
vitamin D	X09035	20	477	•	789	φ
vitamin D	X09036	20	450	٠	789	œ
vitamin D	Y09064	20	427	٠	789	7
an vitamin D r	W68156	19	427	٠.	789	ģ
vitamin D	W47509	19	423	٠	798	'n
amin D rec	W94623	20	423	٠	801	4
Xenopus orphan rec	R98521	17	386		979.5	ίω

ALIGNMENTS

Y09515; Y09515 standard; Protein; 437 AA. 16-JUL-1999 (first entry)

Human vitamin D receptor related gamma protein.

Human; vitamin D receptor related protein; VDRR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia; hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour; hyperproliferative skin disorder; hyperthyroidism.

Homo sapiens.

31-MAR-1998; 14-OCT-1997; 31-AUG-1998; 22-APR-1999. WO9919354-A1. 98SE-0001148 97SE-0003745. 98WO-SE01548

Berkenstam A, Dahlberg M; (PHAA) PHARMACIA & UPJOHN AB

WPI; 1999-302508/25. N-PSDB; X56242.

New vitamin D receptor related (VDRR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a human vitamin D receptor related (VDRR) copypeptide. Human VDRR polypeptides and substances which affect VDRR crimal transduction, can be used for treating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a medicament for treating the following conditions: obesity, diabetes, anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or hyperlipoprotein amid osteoporosis, rheumatoid arthritis, benign and malign tumours, hyperproliferative skin disorders or hyperthyroidism.

Nucleic acid vectors encoding for expression of a VDRR polypeptide can be used for treating metabolic, proliferative or inflammatory conditions, by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or antagonist can be used for the manufacture of a medicament for treating metabolic, proliferative or inflammatory condition.

N.B. The specification specifically claims the VDRR nucleic acid and polypeptide sequences given in figures 1, 4, 7 and 8, but no figures or are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rne present sequence is polypeptide. Human VDRR signal transduction
Human; intranuclear receptor protein; drug development; diagnosis;
                                A human intranuclear receptor protein.
                                                                       04-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Page 19-20; 35pp; English.
                                                                                                                                        Y15931 standard; Protein;
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                                                                                                                                                                                                                                  421
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1 ATPIMQELFGITGS
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N-PSDB; X59975.
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e nucleic acid sequence was isolated from a human adult cDNA
brary using a swellfish ANO23 derived probe. The protein can
used for the development of drugs and diagnosis and treatment
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Pred. No. 1.6e-218;
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12-DEC-1997;
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                      GCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLL
                                                                                                                      RRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTESHFKNFRLPGVLSS
                                                                                          rralikrkksertgtqplgvqglteeqrmmirelmdaqmktfdttfshfknfrlpgvlss
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97US-0069401.
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Pred. No. 1.7e-218;
1; Mismatches 0;
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40

Query Match Best Local S Matches 433

Similarity

99.9**%**; 99.8**%**;

Score 2287; DB 20; Pred. No. 1.7e-218; L; Mismatches 0;

Length

473; 0;

Gaps 60

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Conservative

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                  This invention describes the isolation of the novel human nuclear receptors nR7 or nR7-1. The nR7 and nR7-1 proteins are useful in the identification of downstream target genes and ligands regulating its activity. The nuclear receptor is involved in the regulation of in vivo cell proliferation and/or cell development. The nR7 and nR7-1 polynucleotides, expression vectors and host cells are useful for the recombinant production of the protein.
 Sequence
                                                                                                Claim 20; Fig 6; 80pp; English.
                                                                                                                   DNA encoding human nuclear receptors nNR7
                                                                                                                                       N-PSDB; X78808.
                                                                                                                                                                                                         14-OCT-1998;
12-DEC-1997;
                                                                                                                                                                                                                                                                                                                          nNR7: nNR7-1; nuclear trans-acting receptor protein; human; regulator;
identification; downstream target gene; cell proliferation;
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                                                                                                                                                                                                                                                                                                Homo sapiens.
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473 AA;
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97US-0069401
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                        The present sequence represents a human intranuclear receptor |
The nucleic acid sequence was isolated from a human adult cDNA
library using a swellfish ANO23 derived probe. The protein can
be used for the development of drugs and diagnosis and treatmen
Sequence
                                                                       Disclosure; Page 32-35; 38pp; Japanese.
                                                                                           diagnosis
                                                                                                                                                                                                                                                                                            A human intranuclear receptor protein.
                 of various
                                                                                          New intranuclear receptor protein - useful diagnosis and treatment of disease
                                                                                                                       N-PSDB;
                                                                                                                                WPI; 1999-350330/30.
                                                                                                                                                                      11-AUG-1997;
                                                                                                                                                                                        07-AUG-1998;
                                                                                                                                                                                                                            JP11127872-A.
                                                                                                                                                                                                                                                                                                                                  Y15936;
                                                                                                                                                   (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                          18-MAY-1999.
                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                  treatment.
                                                                                                                                                                                                                                                                         Human; intranuclear receptor protein; drug development; diagnosis;
                                                                                                                                                                                                                                                                                                                04-AUG-1999
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                  diseases.
473 AA;
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Query Match Best Local Similarity

99.98; 99.88;

Score Pred.

2287; No. 1.

1.7e-218;

Length 473;

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RESULT
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The present sequence represents a human intranuclear receptor processes acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment of various diseases.
                                                       Claim
                                                                        New intranuclear receptor protein - useful for drug development diagnosis and treatment of disease
                                                                                                    N-PSDB;
                                                                                                           WPI; 1999-350330/30.
                                                                                                                                                                                                                                                  Human; intranuclear receptor
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| atplmqelfgitgs
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WPI; 1999-302508/25
N-PSDB; X56243.
                                                                                                                                                                                                 Human; vitamin D receptor related protein; VDRR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia;
                               Berkenstam A,
                                                 (PHAA ) PHARMACIA & UPJOHN
                                                                     31-MAR-1998;
14-OCT-1997;
                                                                                                  31-AUG-1998;
                                                                                                                                         WO9919354-A1
                                                                                                                                                            Homo sapiens
                                                                                                                                                                              hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; hyperproliferative skin disorder; hyperthyroidism.
                                                                                                                                                                                                                              Human vitamin D receptor related gamma 2 protein
                                                                                                                                                                                                                                                   16-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                             PHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCELPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKGFFRRAMKRNARLRCPFRKGACEIIRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt rralikrkksertgtqplgvqgiteeqrmmirelmdaqmktfdttfshfknfrlpgvlss}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ckgffrramkrnarlrcpfrkgaceitrktrrqcqacrlrkclesgmkkemimsdeavee
                                                                                                                                                                                                                                                                                                                                       atplmqelfgitgs 473
                                                                                                                                                                                                                                                                                                                                                 ATPLMQELFGITGS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt phmadmstymfkgiisfakvisyfrdlpiedqisllkgaafelcqlrfntvfnaetgtwe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcelpeslgapsreeaakwsgvrkdlcslkvslqlrgedgsvwnykppadsggkeifsll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473
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                                                                                                                                                                                                                                                   (first entry)
                               Dahlberg M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                     98SE-0001148.
97SE-0003745.
                                                                                                  98WO-SE01548
                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.98;
                                                                                                                                                                                                                                                                                         473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2287; DB 20;
Pred. No. 1.7e-218;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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The present sequence is a human vitamin D receptor related (VDRR) CC polypeptide. Human VDRR polypeptides and substances which affect VDRR CC signal transduction, can be used for treating metabolic, proliferative CC or inflammatory: conditions. They can be used in the manufacture of a CC medicament for treating the following conditions: obesity, diabetes, CC anorexia, lipoprotein defects, hyperlipidaemia, hyperchalestarolaemia or CC hyperlipoprotein defects, hyperlipidaemia, hypercholesterolaemia or CC milign tumours, hyperproliferative skin disorders or hyperthyroidism. CC Nucleic acid vectors encoding for expression of a VDRR polypeptide can CC with the can introducing them into a mammal. The introduced nucleic acid is then CC capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or can be used for the manufacture of a medicament for treating metabolic, proliferative or inflammatory condition.

CC N.B. The specification specifically claims the VDRR nucleic acid and CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19; Page 22-24; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vitamin D receptor related (VDRR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating obesity,
473 AA;
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Matches 433;
460
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                                                                                                                                                                                                                                               61 CKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEE 120
                                                                                                                                                                                                                                                                             40 levrpkeswnhadfvhcedtesypgkpsvnadeevggpq1crvcgdkatgyhfnvmtceg
                                                                                                                                                                                                                                                                                      1 MEVRPKESWNIJADFVHCEDTESYPGKPSVNADEEYGGPQICRYCGDKATGYHFNYMTCEG
                                                                          ATPROCELEGITGS 434
atplmqelfgitgs 473
                                     VVDQLQEQFAITLKSY1ECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPF
                                                                                                                                                                                              RRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSS 180
                                                                                                                                                                                                                                      {\tt ckgffrramk:} narlrcpfrkgaceitrktrrqcqacrlrkclesgmkkemims deavee
                                                                                                                                                                                                                                                                                                                  99.9%;
ilarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                  <u>-</u>
                                                                                                                                                                                                                                                                                                                   Score 2287; DB 20;
Pred. No. 1.7e-218;
1; Mismatches 0;
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Query Match Best Local Similarity

Length 473;

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RESULT Y21799 ID Y2 XX AC Y2 XX DT 14

14-SEP-1999 Y21799; Y21799

(first entry)

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standard;

Protein; 434

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Human

steroid and xenobiotic receptor (SXR).

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CC transcription through response elements present in steroid-inducible P450
CC genes, in response to a wide variety of natural and synthetic steroid
CC hormones and (iv) is prominently expressed in liver and intestine. SXR
CC regulates expression of catabolic enzymes, in response to many different
CC steroids, and thus affects metabolism. SXR is a broad specificity, low-
CC affinity receptor for reducing excessive levels of steroids in the
CC circulation. (Ant)sponists of SXR are used to regulate metabolism of
CC steroids particularly phytoestrogens or calcium-channel blockers, to
CC reduce steroid toxicity in subjects being treated with steroids, e.g. in
CC cases of tuberculosis (treated with rifampin and related compounds),
CC breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis
CC (treated with Vitamin K), or to slow metabolism of therapeutic steroids.
CC (treated with Vitamin K), or to slow metabolism of therapeutic steroids.
CC (also, modulating endogenous SXR is used to treat disease, particularly
CC an agonist is used where endogenous steroid levels are excessive (e.g.
CC (cushing syndrome; virilism and hirsutism in women; polycystic ovarian
CC dehydrogenase deficiency, or breast, colorectal or prostatic cancer),
CC while antagonists are used where endogenous steroid levels are too low.
CC cells that express SXR are used to identify compounds likely to be
CC involved in undesirable drug interactions. Antibodies specific for SXR
CC expression density of SXR, also for diagnosis and therapeutically as
CC expression density of SXR, also for diagnosis and therapeutically as
    Matches 415;
                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear receptor; SXR, steroid and xenobiotic receptor; RXR; human; retinoid X receptor; P450 gene; steroid normone; steroid metabolism; phytoestrogen; calcium-channel blocker; steroid toxicity; tuberculosis; breast cancer; osteoporosis; Cushing syndrome; virilism; hirsutism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SXR (steroid and xenobiotic receptor). SXR (1) forms a heterodimer with retinoid X receptor (RXR), (11) binds to a direct or inverted repeat response element motif based on the half-site AGTTCA, (111) activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 1A; 83pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New steroid and xenobiotic receptor, used to identify modulators for controlling metabolism of steroids and xenobiotics, e.g. reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blumberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel nuclear receptor polypeptide, designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-419349/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SALK ) SALK INST BIOLOGICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxicity
                       Similarity
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                                                                                                        434 AA;
                                                                                                                                            The present sequence represents SXR
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease; cancer; colorectal; prostatic.
                   94.7%;
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Score 2169; DB 20;
Pred. No. 7.7e-207;
3; Mismatches 16;
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                                                                                                                                            polypeptide.
                                          Length
    Indels
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MEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEG 60

The invention provides an isolated human nuclear receptor (designated pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase (CYP) promoter. The hPXR is used to identify: its specific modulators, and compounds that induce CYP3A4 expression (i.e. to identify drug interactions, since CYP3A4 is involved in many biotransformations of drugs). The modulators are potentially useful for: associating particular diseases and conditions with PXR and for treating such conditions.

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Human; nuclear receptor; pregnane X receptor; PXR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
Claim 4; Fig 1A-D; 69pp; English.
                                 New human pregnane {\bf X} receptor, used to identify specific modulators and agents that induce expression of cytochrome P-450 mono-oxygenase -
                                                                                                               WPI;
                                                                                                                                                 Kliewer SA,
                                                                                                                                                                                                                                                                 26-MAR-1999;
                                                                                                                                                                                                                                                                                                    30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                          WO9948915-A1.
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y42691 standard; Protein; 414 AA.
                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pregnane X receptor
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                                                                                                                                                   Willson
                                                                                                                                                                                                                            .6656200-SD86
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                                                                                                                                                                                                                                                                                                                                                                                                                mono-oxygenase; drug interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (hPXR).
                                                                                                                                                                                                                                                                                                                                                                                                                    CYP; CYP3A4;
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Best Local Similarity
Matches 413; Conserv
       WPI; 1999-601202/51
                          Kliewer SA, Willson TM;
                                                              27-MAR-1998;
                                                                                 26-MAR-1999;
                                                                                                   30-SEP-1999.
                                                                                                                      WO9948915-A1
                                                                                                                                         Homo
                                                                                                                                                                  Human; nuclear receptor; pregnane X receptor; PXR; CYP; cytochrome P-450 mono-oxygenase; drug interaction; hPXR
                                                                                                                                                                                            His6-pregnane X receptor (PXR) sequence
                                                                                                                                                                                                                17-JAN-2000
                                                                                                                                                                                                                                   Y42689;
                                                                                                                                                                                                                                                     Y42689 standard; Protein; 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies raised against hPXR can be used for determination and purification of hPXR. The present sequence represents the hPXR.
                                           (GLAX ) GLAXO
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401 atplmqelfgitgs 414
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                                                                                                                                      sapiens
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                                                       99WO-US06737. What was 98US-0079593.
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                                                                                                                    Key
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                                                                            Domain
                                                                                                      Domain
                                                                                                                                           Xenopus laevis.
                                                                                                                                                                    hydroxybenzoate; mercaptobenzoate; aminobenzoate
                                                                                                                                                                                  Xenopus orphan receptor 6; XOR-6; steroid receptor; vitamin
                                                                                                                                                                                                           Xenopus orphan receptor 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                              370 AITLKSYIECNRPQPAHRFLFLKIMAMLIELRSINAQHTQRLLRIQDIHPFATFLMQELF 429
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305; Conserv
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100.0%; Pr
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Matches 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 27-28; 42pp; English
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          Rat vitamin D receptor protein VDR0
                                                                            W94623 standard; Protein; 423 AA.
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                                                                                                                                                                                                                                                                                             AKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIIS 256
                                                                                                                                                                                                                                                                                                                                          PLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEA 196
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)B; T36499.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene for vitamin D receptor isoform protein which blocks vitamin D signal pathway - and production of recombinant isoform protein using it, for bone density assay and for screening compounds for vitamin D
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pgshqlyakmiqkladlrslneehskqyrslsfqpensmkltplvlevfg
                                               PAHRELFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPE-ATPLMQELFG 430
                                                                                                                                                                                                                                                                    LPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT---AGGFQQLLLEPM
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                                                                                                    ikfqvglkklnlheeehvllmaicivspdrpgvqdaklveaiqdrlsntlqtyircrhpp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 423;
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RESULT 15
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XX W47509
XX W47509
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.8
Best Local Similarity 42.0
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (VDR1). The isoform differs from the normal receptor (VDR0), which comprises the present sequence, in having the vitamin D response element curtailed by 86 residues, and having an extra 19 residues inserted at the C-terminal of this element. It acts as a dominant negative receptor in the vitamin D signal transmission channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; vitamin D receptor; isoform protein; VDR1; VDR0; diagnosis; dominant negative receptor; signal transmission channel; bone density disorder; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A novel cDNA sequence encodes the rat vitamin D receptor isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 46pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a vitamin D receptor isoform protein - useful for bone density determination and for screening substances for vitamin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-051917/05
N-PSDB; V03129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI PHARM CO LTD (CHUS ) CHUGAI SEIYAKU KK.
   212
                                                                   139
                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                              38 PQICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 97
                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isoform protein can be used to diagnose bone density disorders, screen for substances having potential vitamin D-like activity.
                                                                                                                          QMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAPSREEAAKWSQVRKDLCSLKV---- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ģ
   ----SIQIRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRD 266
                                                                hhktydptyadfrdfrppvrmdgstgsyspr----ptlsfsgnssssssdlyttsldmme 194
                                                                                                                                                                                 rlkrcvdigmmkefiltdeevqrkremimkrkeeealkdslrpk-lseeqqhilaillda 138
                                                                                                                                                                                                                                                 RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 157
                                                                                                                                                                                                                                                                                                                 pricgvcgdratgfhfnamtcegckgffrrsmkrkalftcpf-ngdcritkdnrrhcqac 79
                                                                                                                                                                                                                       Ueno K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     34.8%; Score 798; DB 19;
42.0%; Pred. No. 7.9e-71;
tive 74; Mismatches 136;
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370 pgshqlyakmiqkladlrslneehskqyrslsfqpensmkltplvlevfg 419
                    384 PAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG 430
                                                                                                                                 250 ltsddqivllkssaievimlrsnqsftmddmswdcgsqdykydvtdvskaghtleliepl 309
                                                                                  324 LKFHYMLKKLOLHEEEYYLMQAISLFSPDRPGYLQHRVVDQLQEQFAITLKSYIECNRPQ 383
                                                                                                                                                                                                     195
                                                             sgfsnldlngedsd----dpsvtldlsplsmlphladlvsysiqkvigfakmipgfrd
                                                                                                                                                                  LPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSYCLEDT---AGGFQQLLLEPM 323
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Search completed: February 18, 2001, 14:29:39 Job time: 8216 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                   469.5
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
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Gapop 10.0 , Gapext 0.5
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2290
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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                                                                                                                               US-08-459-489-10
US-08-458-686-10
US-07-843-550C-10
US-07-737-736B-4
US-08-330-283-2
US-08-646-248-2
PCT-US95-13931-2
US-08-342-411A-2
US-08-333-358-8
US-08-333-358-8
US-08-373-652-3
PCT-US95-16311-4
US-08-372-652-1
PCT-US95-16311-1
US-08-372-652-1
PCT-US95-16311-1
US-08-372-652-1
PCT-US95-16311-1
US-08-372-652-1
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5223606-2
   US-09-144-759-18
US-09-144-759-20
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                                                              Sequence 2, Appli
Sequence 2, Appli
Patent No. 5223606
Patent No. 5223606
                                                                                                                                   Sequence 2, Sequence 2, Sequence 2, Sequence 1, Sequence 1, Sequence 2, Sequen
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	371	371	371	371	371	392	401	401.5	409	413	413	413	413	413	414.5	414.5	418	
er +	16.2	σ	16.2	σ	σ	17.1	17.5	17.5	17.9	18.0	18.0	18.0	18.0	18.0	18.1	18.1	18.3	
	548	548	548	475	475	454	462	403	368	797	797	462	462	462	433	433	410	
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ALIGNMENTS	US-08-694-501-2	US-08-463-694-2	US-08-333-358-2	US-08-465-375-2	US-08-484-200-2	5260432-2	5171671-2	US-08-592-383-4	5223606-3	PCT-US92-02320A-2	US-08-095-728B-2	PCT-US92-02320A-4	US-08-095-728B-4	US-08-592-383-2	PCT-US94-07266-2	US-08-466-120-2	5438126-2	
	Sequence 2, 1	Sequence 2, 1	'n	Sequence 2, I	Sequence 2, 1	Patent No. 526	Patent No. 517	Sequence 4, 1	5	'n	Sequence 2, 1	Sequence 4, 1	Sequence 4, F	Sequence 2, P	Sequence 2, P	Sequence 2, A	Patent No. 543	
	Appli	Appli	Appli	\ppli	Appli	5260432	71671	\pp11	23606	Appli	Appli	Appli	Appli	Appli	Appli	Appl1	5438126	

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RESULT 1
US-08-459-489-10
; Sequence 10, Application No. 5686574
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: linear
US-08-459-489-10
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APPLICANT: David D. Moore et al.

TITLE OF INVENTION: CAR RECEPTORS AND RELATIONED FOR INVENTION: MOLECULES AND METHODS NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
                                                                                               TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMULCATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION UNMEER: 07/843,350
APPLICATION NUMEER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: IBM P.C. DOS (Version SOFTWARE: WordPerfect (Version 5.0) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" D1
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/459,489 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts COUNTRY: U.S.A.
                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PS/2 Model
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2 Model 502 or 55SX
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Query Match 33.5%; Score 768; DB 1; I Best Local Similarity 42.2%; Pred. No. 4.1e-68; Matches 164; Conservative 62; Mismatches 109; Length 348; Indels 54; Gaps

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Š 41 CRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLR 100

Matches 164; Best Local Similarity

Conservative

62;

Pred. No. 4.1e-68;
2; Mismatches 109;

Indels

54;

6,

153

258

42.2%;

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US-08-458-686-10
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                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION NDMBER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WORDPEFFECT (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                         REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                 TYPE: amino acid
STRANDEDNESS: N/F
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                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,162
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                TOPOLOGY:
                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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VENTION: CAR RECEPTORS AND RELATED

VENTION: MOLECULES AND METHODS
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                  linear
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                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PAUL T. Clark
REGISTRATION AUDMER: 30,162
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBH PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: David D. TITLE OF INVENTION: TITLE OF INVENTION:
                                    SEQUENCE CHARACTERISTICS LENGTH: 348
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MEDIUM TYPE: 3.5" Diskette,
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                                                                             TELEFAX: 10-
TELEFAX: 200154
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STRANDEDNESS:
                    TYPE:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/843,350C FILING DATE: February 26, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
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                                  LENGTH:
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                                                                                                               (617) 542-50
(617) 542-8906
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MOLECULES AND
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US-07-843-350C-10
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Best Local :
                    TELEFAX: 414-277-5774
INFORMATION FOR SEQ ID NO:
                                                      APPLICATION NUMBER: US/07/737
FILING DATE: 19910730
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
REFERENCE/DOCKET NUMBER: 96-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION UNIVERS. IS (07.727.727.72)
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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IIILE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
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Local Similarity 42.2%;
tes 164; Conservative 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRSINEAYGYQIQHIQGLSAM-MPLLQEI 346
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ross, Troy K.
Prahl, Jean M.
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ORGANISM: RBT
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Burmester, James K.
AUTHORS: Maeda, No. 5260199uyo
AUTHORS: DeLuca, Hector F.;
TITLE: Isolation and expression of rat
TITLE: 1,25-dihydroxyvitamin D3 receptor cDNA
JOURNAL: erc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-08-330-518-2
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                                                                                                                                                                                                                                                                                                       Sequence 2, ... Patent No. 5
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Best Local (
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                           APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
                                                                                                                                                                                                           APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         350 NSMKLTPLVLEVFG 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 MADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 TLSFSGNSSSSSSDLYTTSLDMMEPSGFSNLDLNGEDSD-----DPSVTLDLSPLSMLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 GTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 LKDSLRPK-LSEEQQHIIAILLDAHHKTYDPTYADFRDFRPPVRMDGSTGSYSPR----P 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 RLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                           STREET:
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COUNTRY:
                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SREEAAKWSQVRKDLCSLKV:-----SLQLRGEDGSVWNYKPPADSGGKEIFSLLPH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPF-ATPLMCELFG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLVEAIQDRLSNTLQTYIRCRHPPPGSHQLYAKMIQKLADLRSLNEEHSKQYRSLSFQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDI 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQDYKYDYTDVSKAGHTLELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LADLVSYSIGKVIGFAKMIPGFRDLTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCG
                                                                                                                                                                                                                                                                                                           ; Application US/08330518
5607967
                                         Rahway
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                  New Jersey
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                                                           126 East Lincoln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%; Score 629; DB 1; Length 367; ilarity 38.5%; Pred. No. 2.6e-54; Conservative 70; Mismatches 132; Indels
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                                                                                Merck & Co., Inc.
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RESULT 6
US-08-330-283-2
; Sequence 2, Application US/08330283
; Patent No. 5679518
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Best Local Similarity 29.0
Matches 126; Conservative
  GENERAL INFORMATION:
APPLICANT: Friedm
APPLICANT: Hollow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283
TELEPHAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 461 amino acid
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NAME: DOLAN, Catherine A.
REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 OCRLRKCKEAGMREOCVLSEEQIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSASGPGA 200
                                                                                                                                                                                      447 -- KKLPPLLSEIWDV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC-- 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 LPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     --GRLSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPQICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95
                                                                                                                                                                                                                          IHPFATPLMQELFGI 431
                                                                                                                                                                                                                                                                     PGRVEALQQPYVEALLSYTRIKRPQDQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD
                                                                                                                                                                                                                                                                                                           HRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQD 416
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELAIISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECIT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPGGSEAGSQGSGEGEGVQLTAAQELMIQQLVAAQLQCNKRSFS-------
                                                                                                                                                                                                                                                                                                                                                   FLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 amino acids
  Friedman, Holloway,
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Eitan
M. Katharine
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MOLECULE TYPE: I

HYPOTHETICAL: NO

NATI-SENSE: NO
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: :Floppy disk
COMPUTER: IBW PC compatible
COMPUTER: PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                 329 FLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQE
                                                                                                                                                                                272 TELAIISVQE:\DFAKQVPGFLQLGREDQIALLKASTIBIMLLETARRYNHET---ECIT 328
                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                                                                                                                                                                                                                                                                                                  143
                   389 PGRVEALQQPYVEALLSYTRIKRPQDQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD
                                                         359 HRVVDQLQEQPAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQD 416
                                                                                                                                                                                                                          244 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC--
                                                                                                                                                                                                                                                                                                       184 LPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 ACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQ---PLGVQG------ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 GHELCRYCGDKASGFHYNYLSCEGCKGFFRRSYYRGGARRYACRGGGTCQMDAFMRRKCQ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 GPQICRVCGDKAIGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dolan, Catherine A. REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US 7 ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rahway
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                          --GRLSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                  QCRLRKCKEAGMREQCVLSEEQIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSASGPGA 200
                                                                                                                                                                                                                                                                     -----DQPKVTPWP-----HF 271
                                                                                                                                                                                                                                                                                                                                               SPGGSEAGSQGSGEGEGVQLTAAQELMIQQLVAAQLQCNKRSFS------
                                                                                                                                                                                                                                                                                                                                                                                       126 East Lincoln Avenue
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Schmidt, Azriel
Vogel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodan, Gideon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.7%; Score 498; DB 1; 29.0%; Pred. No. 3.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHOD FOR FINDING RECEPTOR POTENTIATORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86;
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US-08-646-248-2
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 126; Conserv
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TELEFAX: (908) 594-47
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/3
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                   143 QCRLRKCKEAGMREQCVLSEEQIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSSASGPGA 200
  184 LPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHM 243
                                                                           143 ------LTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 14-MAY CLASSIFICATION: 536
                                     201 SPGGSEAGSQGSGEGEGVQLTAAQELMIQQLVAAQLQCNKRSFS------ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Dolan, Catherine A. REGISTRATION NUMBER: 36,502 REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                    96 ACRIRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQ---PLGVQG------ 142
                                                                                                                                                                                                  83 GHELCRYCGDKASGFHYNYLSCEGCKGFFRRSVYRGGARRYACRGGGTCQMDAFMRRKCQ 142
                                                                                                                                                                                                                                        37 GPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95
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126 East Lincoln Avenue
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Schmidt, Azriel
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Holloway, M. Katharine
Rodan, Gideon
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                                                                                                                                                                                                                                                                              21.7%; Score 498; DB 2; Length 461; 29.0%; Pred. No. 3.6e-41; tive 86; Mismatches 125; Indels
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PCT-US95-13924-2
                                                                                              PCT-US95-13924-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9513924 GENERAL INFORMATION:
                   Query Match 21.7%; Score 498; DB 4; Length 461; Best Local Similarity 29.0%; Pred. No. 3.6e-41;
 Matches 126; Conservative
                                                                                                                                                                                                                                           TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                            MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NC.
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APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 193
TELECOMMUNICATION INFORMATION:
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NAME: Quagliato, Carol S
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 -- GRISYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 TELAIISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECIT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWEC -- 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 PGRVEALQQPYVEALLSYTRIKRPODQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD
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ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                        TOPOLOGY: 111
                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                             461 amino acids
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126 East Lincoln Avenue
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Holloway, M. Katharine
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86; Mismatches
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 125; Indels 98; Gaps
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PCT-US95-13931-2
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GENERAL INFORMATION:
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    TOPOLOGY: 1i
MOLECULE TYPE:
HYPOTHETICAL: 1
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-3809
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13931
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Quagliato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 HRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQD 416
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ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 LPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 SPGGSEAGSQGSGEGEGVQLTAAQELMIQQLVAAQLQCNKRSFS-------
                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELAIISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECIT 328
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                                                                                                                  461 amino acids
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                                                                                                                                                                                 (908)
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126 East Lincoln Avenue
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      peptide
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US-08-342-411A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08342411A Patent No. 5639616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                          APPLICATION NUMBER: US/08/342
FILING DATE: 18 NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT: INFORMATION:
NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                  REFERENCE/DOCKET NUMBER: ARCD154
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTIFIE OF INVENTION: COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LIAO, Shutsung APPLICANT: SONG, Ching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 -- KKLPPLLSEIWDV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 PGRVEALQQP;VEALLSYTRIKRPQDQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 FLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 --GRLSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 TELAIISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECIT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC-- 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 QCRLRKCKEAGMREQCVLSEEQIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSSASGPGA 200
  TELEPHONE:
                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 ACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQ---PLGVQG------ 142
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                                                                                                                                                                                                                                                                                                                                                                                                     Houston
                                                                                                                                                                                                                                                                                                                                                                                                                               P.O. Box 4433
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                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arnold, White & Durkee
(512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UBIQUITOUS NUCLEAR RECEPTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.7%; Score 498; DB 4; 29.0%; Pred. No. 3.6e-41;
                                                                                                                                                                          US/08/342,411A
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US-08-333-358-8
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Best Local Similarity
                                                                                                                                                         APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELLIA S.
APPLICANT: ONG Ph.D., ANTHONY E.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: GIGUERE Ph.D., VINCENT MNN
APPLICANT: TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PYSELY, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application Patent No. 5571696
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                      COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC-- 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 GHELCRYCGDKASGFHYNVLDCEGCKGFFRRSYVRGGARRYACRGGGTCQMDAFMRRKCQ 141
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- KKLPPLLSEIWDV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGRVEALQQPYVEALLSYTRYKRPQDQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD 445
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Patentin Release #1.0, Version #1.25
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; Pred. No. 5.6e-41;
86; Mismatches 125; Indels
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-358-8
                                                                                                                           Sequence 8, Application US/08463694; Patent No. 5596233; GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 8:
                                                                            APPLICANT:
APPLICANT:
                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Reiter Ph.D., Stephen E. REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 --- RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 184
                                                                                                                                                                                                                                                                                                                                                                                   366 QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 VSVQEIVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFN--AETGTWECGRLSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQL 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127;
EYANS Ph.D., RONALD M.
MANGELSBORF Ph.D., DAVID J.
ONG MS., ESTELITA S.
ORO Ph.D., ANTHONY E.
BORGMEYER Ph.D., UWE K.
GIGUERE Ph.D., VINCENT MMN
YAO MI., TSO-PANG MMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/333,358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 491.5; DB 1
Pred. No. 1.5e-40;
5; Mismatches 145
                                                                                                 DAVID J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 440;
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Gaps

12;

TITLE OF INVENTION:

NOVEL RECEPTORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amin
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: US 07/761,06
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Relter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        185 LPPRRSSPPQILPQLSPEQLGMIEKLVAAQQQCNRRSFS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 184
                                                                                     366 QEQFAITLKSYIECNRPQPAHRELELKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 423
                                                                                                                                   315 NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL
                                                                                                                                                                             307 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQL 365
                                                                                                                                                                                                                           256 VSVQEIVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY 314
                                                                                                                                                                                                                                                                  249 YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFN--AETGTWECGRLSY 306
                                                                                                                                                                                                                                                                                                                224 ---DRLRVTPWPMAP------ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 ---RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESL 188
    424 LMQELFGI 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/463,694 FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
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                                                                                                                                                                                                                                                                                                                                                            QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 131
                                              QHTYYEALHAYYSIHHPH--DRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPTEIRPOKRKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGAHYIC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Pretty, Schroeder, Brueggemann & Clark 444 So. Flower St., Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.5%; Score 491.5; DB 1; 29.7%; Pred. No. 1.5e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match .21.5%; Score 491.5; Best Local Similarity 29.7%; Pred. No. 1.56 Matches 127; Conservative 85; Mismatches
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION HUMBER: 31192
REFERENCE/DOCKET NUMBER: 931 893
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONC MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UME K.
APPLICANT: GIGUERE Ph.D., VINCENT MMN
APPLICANT: YAO, Mr., TSO-PANG MMN
TITLE OF INVENTION: NOVEL RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                         249
                                                                     224 ---DRLRVTPWPMAP---
                                                                                                                                                                                                                                                128 -HSGGHCPMDFYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 184
                                                                                                                                                                                                  132 ---RTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESL 188
                                                                                                                                                                                                                                                                                                                                      68 EPTEIRPQKRKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGAHYIC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: US/07/761,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 444 So. F
CITY: Los Angeles
                                                                                                                                                                                                                                                                                          78 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 131
                                                                                                                                                                                                                                                                                                                                                                                  18 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/694,501 FILING DATE: 107-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFN--AETGTWECGRLSY 306
                                                                                                                                                        LPPRRSSPPQILPQLSPEQLGMIEKLVAAQQQCNRRSFS------ 223
                                                                                                            QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8, Application US/08694501
5, 5710004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 1;
                                                                   --DPHSREARQQRFA---HFTELAI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 440;
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US-08-373-935-1
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.,
127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
192 LPPRRSSPPQILPQLSPEQLGMIEKLVAAQQQCNRRSFS----
                                                                              135 -HSGGHCPMDTYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAHATS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: IDENTIFICATION OF A DISTINCT
TITLE OF INVENTION: RETINOID-RESPONSIVE PATHWAY AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                  132 ---RTGTOPLGYQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGYLSSGCELPESL 188
                                                                                                                                                                                     18 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 77
                                                                                                                        78 PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE----- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4. CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 VSVQEIVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 LLSEIWDV 438
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/373,935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 9007
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                               EPTEIRPOKRKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGAHYIC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHTYVEALHAYVSIHHPH--DRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP 430
                                                                                                                                                                                                                                                                                                                                                                                                                                          447 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pretty, Schroeder, Brueggemann & Clark 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mangelsdorf, David J. Willy, Patricia J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans, Ronald M.
                                                                                                                                                                                                                                                21.5%; Score 491.5; DB 1; Length 447; 29.7%; Pred. No. 1.5e-40; ative 65; Mismatches 145; Indels 71.
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                                                                                                          Query Match
Best Local Similarity
                                                                                         Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5932699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentID Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,652
FILING DATE: '13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark .Paul T.
NAME: Clark .Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sec1, Wong1
APPLICANT: Cho1, Hueng-Sik
TITLE OF INVENTION: REFINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
74 GHELCRYCGDKASGFHYNYLSCEGCKGFFRRSYVHGGAGRYACRGSGTCQMDAFMRRKCQ 133
                     37 GPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95
                                                                                                                                                                                                                              LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 LLSEIWDV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 LMQELFGI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFN--AETGTWECGRLSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 VSVQEIVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 ---DRLRVTFWPMAP------ 262
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QHTYVEALHAYVSIHHPH--DRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 Franklin Street, Suite 3100
                                                                             Conservative 84; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore, David
                                                                                                                                                                                                                                                   not relevant
                                                                                                    21.4%; Score 490; DB 2; Length 446; 29.1%; Pred. No. 2.1e-40;
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	•	436 PLLSEIWDV 444	436	В
	·····•	PLMQELFGI 431	423	Qy
43	380 LQQPYVEALLSTIRIKRPQDQLRFPRMLMKLVSLRTLSSVHSEQVFALRLQDKKLP 43	LOOPYVEALLSY	380	В
42	365 LQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFAT 42	LQEQFAITLKSY:	365	φ
37	320 YSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPSRVEA 37	YSKDDFHRAGLQV	320	뭥
36	YCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQ 36	YCLED-TAGGFQ	306	Qγ
32	263 SVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLQTARRYNHETECITFLKDFT 31	SVQEIVDFAKQVI	263	В
30	250 MFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLS 30	MFKGIISFAKVIS	250	Qy
26	230DQPKVTPWPLGADPQSRDARQQRFAHFTELAII 26	DQPKVTPWP	230	Ф
24.0	APSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHWADMSTY 24:	APSREEAAKWSQV	190	Qy
22	192 ASSOGSGEGEGIQLTAAQELMIQQLVAAQIQCNKRSFS	ASSÓGSGEGEGIO	192	ర్థ
189	138 LGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQ 18:	LGVQG	138	Qy
191	134 LCRLRKCKEAGMREQCVLSEEQIRKKRIQKQQQQQPPPPSEPAASSGRPAASPGTSE 19:	LCRLRKCKEAGME	134	Вb
137	96 ACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQP 13;	ACRLRKCLESGMK	96	Qγ

Search completed: February 18, 2001, 14:31:58 Job time: 6201 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2001, 12:06:00 ; Search time 51.75 Seconds (without alignments) 270.834 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-143-8282 2290 1 MEVRPKESWNHADEVHCEDT.....QDIHPFATPLMQELFGITGS 434

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

88757 seqs, 32294092 residues

Searched:

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum-Match 08

1008

Listing first 45 summaries SwissProt_39

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by enalysis of the total score distribution.

SUMMARIES

(J.	32	31	30	29	. 28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	on	ហ	4	w	N	ם	Regult No.
434	437	437	441	441	442	443	444.5	445	448	449	450	450	455.5	487	æ	9	496.5	498	498.5	725	729	768	789	789	792.5	801	814	815	1.0	61.	79.	229	Score
19.0	19.1		19.3						19.6					:	21.4	21.5	21.7	:	21.8	:	:	•	•	·				35.6	. 1	16	77.7	Õ	Match
416 1	514 1							476 1		373 1	461 1	369 1	395 1	446 1	446 1	447 1	445 1	461 1	445 1	358 1	358 1	348 1	427 1	424 1	422 1	423 1	422 1	451 1	448 1	431 1	431 1	434 1	ength DB
THAA_PAROL	THB2_RAT	THB1_RAT	THB2_MOUSE	. THB1_MOUSE	EG	THBE	ECR_LOCCO	THB2	THBA	THB_RANCA	THB1_HUMAN	THB_CHICK	THB_PAROL	NRH2_RAT	. NRH2 MOUSE	. NRH3_HUMAN	. NRH3_RAT	NRH2_HUMAN	SDOW	. NRI3_MOUSE	. NRI3_RAT			VDR_BOVIN	VDR_MOUSE	VDR_RAT	VDR_XENLA	VDR_CHICK	VDR_COTJA		PXR_MOUSE	PXR_HUMAN	3 ID
Q91241	P37826	P18113	P37244	P37242	P49880	P18119	018531	P37243	P18117	Q02965	P10828	P18112	Q91279	Q62755	260644	Q13133	Q62685	P55055	Q9z0y9	035627	Q9qus1	Q14994	P11473	Q28037	P48281	P13053	013124	042392	P49701	Q9rla7	054915	075469	Description
paralic	rattus	ratt	mus	mus mu	aedes ae		luci	homo san	xeno	rana				ratt	mus n	рğ	rattu	homo	mus		rattu	homo sapie	рошо	809	mus mus	rattus n	xenopu	gallus ge	coturns	ratt	mus m	homo sap	

255555

EMBL; AF061056; AAD05436.1; -.
EMBL; AF084645; AAC64558.1; -.
MIM; 603065; -.
INTERPRO; IPR000324; -.
INTERPRO; IPR000536; -.

ALIGNMENTS

INTERPRO; IPR001628; -. INTERPRO; IPR001723; -.

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PXR_MOUSE
ID PXR_M
AC 05491
DT 15-JU
DT 15-JU
DT 01-OC
DE ORPHA
GN NR112
OS MUS M
OC EUKAR
OC Manma
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RP SEQUE
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Matches 434
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ZN_FING
ZN_FING
DOMAIN
                                                                                                       PXR_MOUSE STANDARD; PRT; 431 AA. 054915; 05-915 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) 0RPHAN NUCLEAR RECEPTOR PXR (PREGNANE X RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
 MEDLINE-98149345; PubMed-9489701; Kliewer S.A., Moore J.T., Wade L., S. Jones S.A., McKee D.D., Oliver B.B.,
                                 TISSUE-LIVER;
                                           SEQUENCE FROM N.A., AND
                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                      Mus musculus (Mouse).
                                                                                                   NR1I2 OR PXR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                    ATPLMQELFGITGS 434
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                                                                                                                                                                                                                        ATPLMQELFGITGS
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                                                                                                                                                                                                                                                                                                            CGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                 Chordata;
Rodentia;
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                                            ALTERNATIVE SPLICING
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C4-TYPE.
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1DF6A2AE3109C4DA
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Pred. No. 1.3e-176;
                                                                 Craniata; Vertebrata; 1
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
  ., Willson T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; Nuclear
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   Zetterstrom R.H.,
                                                                    Euteleostomi; 
; Murinae; Mus
            Watson M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434;
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MGD; MGI:1337040; NR1I2.
INTERPRO; IPR000324; --
INTERPRO; IPR000536; --
INTERPRO; IPR001528; --
INTERPRO; IPR001723; --
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ZN_FING
ZN_FING
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DOMAIN
VARSPLIC
SEQUENCE
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Cell 92:73-82(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; Transcription regulation; DNA-binding; Nuclear
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                        303
                                                                                                                                                                       180
                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ORPHAN RECEPTOR; ITS NATURAL LIGAND IS PROBABLY PROGNAME. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTEI SUBUNIT: FORMS A HETERODIMER WITH RXR.
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PXR.1 (SHOWN HERE) AND 2/PXR.2; ARZ PRODUCED BY ALTERNATIVE SPLICING.
INDUCTION: ACTIVATED BY NATURALLY OCCURRING STEROIDS SUCH AS PREGNENOLONZ AND PROGESTERONE, SYNTHETIC GLUCCORTICOIDS AND ANTIGLUCCOCRTICOIDS AND 16-ALPHA-CARBONITRILE (PCN).
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                      RLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVV
                                                                                              MADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECG
                                                                                                                                                                                                                                                              ELPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPH
                                                                                                                                                                                                                                                                                                                                                                                      GFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRPEESWSRVGLVQCEEADSALEEP-INVEEEDGGLQICRVCGDKANGYHFNVMTCEGCK
                                                                                                                                                                                                                                                                                                                                                               GFFRRAMKRNVRLRCPFRKGTCEITRKTRRQCQACRLRKCLESGMKKEMIMSDAAVEQRR
PR00350; VITAMINDR.

PR00398; STRDHORMONER.

PR00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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38
74
105
202
171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternative splicing
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58
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201
431
211
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77.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1779.5;
Pred. No. 1.3e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGAND-BINDING.
MISSING (IN ISOFORM
; F592AF91F689329E C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HINGE
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.3e-1
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55;
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CRC64;
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                                                Query Match
Best Local S
Matches 330
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INTERPRO; IPRO00536; -...
INTERPRO; IPRO01628; -...
INTERPRO; IPRO01723; -...
PRAM; PPO0104; hormone_rec; 1.
PPAM; PPO0105; zf-C4; 1.
PRINTS; PRO0047; STROUDFINGER.
PRINTS; PRO00350; VITAMINDR.
                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                 ZN_FING
                                                                                                                                                                               ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang H., LeCulyse E., Liu L., Hu M., Matoney L., Zhu W., Rat pregnane X receptor: molecular cloning, tissue distresemblotic regulation.";
Arch. Biochem. Biophys. 368:14-22(1999).
-I- FUNCTION: ORPHAN RECEPTOR; ITS NATURAL LIGAND IS PROBPREGNANE. BINDS TO A RESPONSE ELEMENT IN CYPJA GENES
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF151377; AAD47214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
0RPHAN NUCLEAR RECEPTOR PXR (PREGNAME X RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NR112 OR PXR.
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                                                                                                                                                                                                         inc-finger.
                                                                                                                                                                                                                      Receptor; Transcription
                                                                                                                                                                                                                                     ROSITE; PS00031;
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SUBUNIT: FORMS A HETERODIMER WITH RXR (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLMQELFGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLAYCFEDPNGGFQKLLLDPLMKFHCMLKKLQLHKEEYVLMQAISLFSPDRPGVVQRSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLMQELFSST
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                                                                                                                                                                                                                                             PR00350; VITAMINDR.
PR00398; STRDHORMONER.
                                                              Similarity
                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432
                                                                                                                                                                                                                  NUCLEAR_RECEPTOR; 1.
iption regulation; DNA-binding; Nuclear protein;
                                                                                                                                  104
58
99
201
431
                                                                                                                    49660 MW;
                                                            76.98;
76.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                             42;
                                                                                                               C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
HINGE.
LIGAND-BINDING.
W; 4B545F21F9439697 CRC64;
                                           Score 1761.5; DB 1;
Pred. No. 3.6e-134;
2; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 AA
                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / L., Zhu W., Yan B.;
tissue distribution,
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS PROBABLY
                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROMOTER
                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus.
                                          Gaps
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EMBL; U12641; AAA56725.1; HSSP; P03372; 1HCQ.

THCO.

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COTJA
                                                                                                                                                                                                                                                    PROC. Natl. Acad. Sci. U.S.A. 91:11596-11600(1994).

-I FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE EXPRESSION OF HORMONE SENSITIVE GENES.
-I SUBCELLULAR LOCATION: NUCLEAR.
-I ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-I DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.
-I DOMAIN: COMPOSED OF THREE DOMAINS THE STROID-BINDING DOMAIN.
-I SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDR_COTJA
P49701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-CHORIOALLANTOIC MEMBRANE;
MEDLINE-95062315; PubMed-7972109;
MEDLATOUSSI M.A., 'Prahl J.M., Deluca H.F.;
"The avian vitamin D receptors: primary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coturnix coturnix japonica (Japanese quail).

Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   origins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELPESIQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Best Local
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                                                                                                                                                                                                VDR_CHICK STANDARD; PRT; 451 AA.
042392;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00047; STROIDFINGER. PRINTS; PR00350; VITAMINDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00104; hormone_rec; PFAM; PF00105; zf-C4; 1.
                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-LEGHORN; TISSUE-KIDNEY;
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                                                                                                                                                                                  VDR OR NR111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 CEDTE --- SVPGKPSVNADE - EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP-------GVL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLR 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQPEHSMQLTPLVLEVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 815.5; DB 1
Pred. No. 3.3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VITAMIN D3 RECEPTOR, VITAMIN D3 RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGAND-BINDING
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INTERPRO; IPRO00536; -.
INTERPRO; IPRO01628; -.
PRAM; PF00104; hormone_rec; 1.
PRAM; PF00105; Zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR000350; VITAMINDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 235:1214-1217(1987).

-I - FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTITUE EXPRESSION OF HORMONE SENSITIVE GENES.
-I- SUBCELLULAR: LOCATION: NUCLEAR.
-I- ALTERNATIVE: PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McDonnell D.P., Mangelsdorf D.J.,
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Lu Z., Hanson K:, Deluca H.F.;
"Cloning and origin of the two forms of chicken vitamin D receptor.";
Arch. Biochem. Biophys. 339:99-106(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Transcription Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for vitamin D.
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     182
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                                                                                                                                                       118 VEERRALIKRKKSERTGTQPLGVQGLTBEQRMMIRELMDAQMKTFDTTFSHFKNFRLP-- 175
                                                                                                                                                                                                                64
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TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.

TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DO

A DOMA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

A DIM-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NR1 SUBFAMILY.
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SKFSSRMATHSSSVVSQDFSSEDSNDVFGSDAFAAFPEPMEPQMFSNLDLSEESDESPSM 241
                                                                                                  ------GVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKYSLQLRGEDGSVW
                                                                                                                                                                                                                                                                                                                                                                                                                              181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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VITAMIN D3 RECEPTOR, FORM B.
FOR FORM B.
C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 815; DB 1;
Pred. No. 3.6e-58;
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LIGAND-BINDING.
; 2078B6A6C8D8E5FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the avian receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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   DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                        PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 138:2347-2353(1997).

1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE EXPRESSION OF HORMONE SENSITIVE GENES.

1- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97307679; PubMed-9165021;
L1 Y.C., Bergwitz C., Jueppner H., Demay M.B.;
"Cloning and characterization of the vitamin D receptor from Xenopus
                                                                                       Receptor; Tr
Zinc-finger.
                                                                                                                                                                                                                                                                                                                           INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                           EMBL; U91846; AAB58585.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDR OR NR111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDR_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 NYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST LEVEL IN SMALL INTESTINE AND SKIN.

DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASES GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE LEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEEN IN ADULT.
                                                                                                                                                                                                                             PF00104; hormone_rec; 1. PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLMQAISLESPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLELKIMAMLTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMLRSNOSFTMEDMSWTCGSNDFKYKVSDVTQAGHSMDLLEPLVKFQVGLKKLNLHEEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLRENTVENAETGTWECGR--LSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEY 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY
                                                                                                                                                                                                                                                                                                               IPR000324; -. IPR000536; -.
                                                                                                                Transcription
                                                                                                                                                                                                                                                                                            IPR001628; -.
      61
25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
      850
                                                                                                       AR_RECEPTOR; 1.
regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesobatrachia; Pipoidea;
C4-TYPE ZINC FINGERS (TWO). C4-TYPE. C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          TAN COMMINICATION (RAT).
RATTUS norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Rattus.
This SWISS-PROT entry
                                                                           ÷
                                                                                                                                                                             Burmester J.K., Maeda N.,
                                                                                                                                                                                                                                                                                     Burmester J.K., Wiese
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13,
01-JAN-1990 (Rel. 13,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                              MEDLINE-88124963;
                                                                                                                                                                                                         SEQUENCE OF 58-423 FROM N.A.
                                                                                                                                                                                                                                                                                                 MEDLINE-89071726; PubMed-2849110;
                                                                                                                                                                                                                                                                                                                                                                                             VDR OR NR1I1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P13053
                                                                                                                                                                                                                                                                Jurmester J.K., wiese R.J., Maeda N., Deluca H.;
Structure and regulation of the rat 1,25-dihydroxyvitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDR_RAT
                                                                                                                                                        urmester J.K., Maeda N., Deluca H.F.; Isolation and expression of rat 1.25-dihydroxyvitamin D3 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 KSYIECNRPCPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFA---TPLMQELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 GFQQLLLEPYLKFHYMLKKLQLHEEEYYLMQAISLFSPDRPGYLQHRVVDQLQEQFAITL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 QMKTFDTTFSHFKNFRLÞGVLSSGCELÞESLQAÞSREEAAKWSQVRKDLCSLKVSLQLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 PQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 97
                                                                                 C. Natl. Acad. Sci. U.S.A. 85:1005-1009(1988).
FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN
THE EXPRESSION OF HORMONE SENSITIVE GENES.
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                  DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
                                     SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                               NRI SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTYILCKHPPPGSRLLYAKMIQKLADLRSLNEEHSKQYRSISFLPEHSMKLTPLMLEVF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHNMELLEPLVKFQVGLKKLDLHEEEHVLLMAICILSPDRPGLQDKALVESIQDRLSSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGR--LSYCLED-TAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FARMIPGFRDLIAEDQIALLKSSVIEVIMLRSNQSFSLDDMSWTCGSEDFKYKVDDVTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPSEDSDVFTSSPDSSEHGFFSASLFGQFEYSSMGGKSGELSMLPHIADLVSYSIQKIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EDGSVWNYKPPADS---------GGKE-IFSLLPHMADMSTYMFKGIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLRKCLESGYKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRYMIRELMDA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICGYCGDKATGFHFNAMTCEGCKGFFRRSMKRKAMFTCPF-NGDCRITKDNRRHCQSC 80
                                                                                                                                                                                                                                         Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLKRCVDIGMMKEFILTDEEVQRKRQMINKRKSEEALKESMRPK-ISDEQQKMIDILLEA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189
422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                         PubMed=2829212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
422
48188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 814; DB 1;
Pred. No. 4e-58;
                                                                                                                                                                                                                                     85:9499-9502(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C8A9F25414FEE9D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00104; hormone_rec; 1. PFAM; PF00105; zf-C4; 1. PR1NTS; PR00047; STROIDFINGER. PRINTS; PR00350; VITAMINDR.
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                                                                                                                                                                      VDR_MOUSE P48281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
15-JUL-1999 (Rel. 38, Last ann
VITAMIN D3 RECEPTOR (VDR) (1,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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     musculus (Mouse)
                                  OR NR1I1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A31761; A31761.
A31367; A31367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAPSREEAAKWSQVRKDLCSLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKFHYMLKKLQLHEEEYVLMQAISLESPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDVTDVSKAGHTLELIEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT---AGGFQQLLLEPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHKTYDPTYADFRDFRPPVRMDGSTGSYSPR----PTLSFSGNSSSSSSDLYTTSLDMME
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                                                                                                                                                                                                                                                                                                                                                                                        PAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG 430
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                                                                                                                                                                                                                                                                                                                                     PGSHQLYAKMIQKLADLRSLNEEHSKQYRSLSFQPENSMKLTPLVLEVFG
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); IPRO00324; -.
); IPRO00536; -.
); IPRO01628; -.
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24 89 C
24 44 C
60 84 C
90 187 H
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                                                                                                                                                                                                   STANDARD;
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84 C
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423 I
47813 MW;
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42.0%; Pred. No. 4.5e-57;
                                                         Last sequence update)
Last annotation update)
VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75;
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C4-TYPE.
HINGE.
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1A0E519A9DCCE990 CRC64;
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Best Local :
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MGD; MGT:103076; VDR.
INTERPRO; IPR000324; -.
INTERPRO; IPR000536; -.
INTERPRO; IPR001028; -.
EPRAM; PF00104; hormone_rec; 1.
PFRAM; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN THE EXPRESSION OF HORMONE SENSITIVE GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor.";
Gene 152:281-282(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kamei Y., Kawadā T., Fukuwatari T., Ono T., Kato "Cloning and sequencing of the gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM NA.
MEDLINE-95137405; PubMed-7835717;
Kamei Y., Kawada T., Fukuwatari T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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PRINTS; PR00350; VITAMINDR
PROSITE; PS00031; NUCLEAR_RECEPTOR;
RECEPTOR; Transcription regulation;
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                                                                                           261
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DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.

A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NR1 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
ELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAKLVEAIQDRLSNTLQTYI 362
                           LLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLOEQFAITLKSYI 377
                                                                                                                        TM--DL-----NEEGS----DDPSVTLDLSPLSMLPHLADLVSYSIQKVIGFAKM
                                                                                                                                                                                                             OMKTFDTTFSHFKNFRLP--GVLSSGCELP------ESLQAPSRE--EAAKWS 200
                                                                                                                                                                                                                                                                          RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 157
                                                                                                                                                                                                                                                                                                          PRICGYCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC 79
                                                                                                                                                                                                                                                                                                                                       POICRYCGDKATGYHFNYMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC
                                                                                                                                                     OVEKDLCSLKYSLOLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKV 260
                                                                                                                                                                                   HHKTYDPTYADFRDFRPPIRADVSTGSYSPRPTLSFSGDSSSNSDLYTPSLDMMEPASFS 198
                                                                                                                                                                                                                                               RLKRCVDIGMMKEFILIDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQQHIIAIILDA 138
                                                           IPGFRDLTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDITDVSRAGHTL 302
                                                                                         ISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT---AGGFQQ 317
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    47851 MW;
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                                                                                                                                                                                                                                                                                                                                                                         74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         Score 792.5; DB 1
Pred. No. 2.2e-56;
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C4-TYPE.
HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGAND-BINDING.; 4704CC8172445732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4-TYPE ZINC

    DNA-binding; Nuclear protein;

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                                                                                                                                                                                                                                                                                                                                                                                                       Length 422;
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ECNRPOPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG

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VDR_BOVID

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
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Melbergs H.L., Bosworth B.T., Reinhardt T.A.;
*Nucleotide sequence of the bovine vitamin D3 receptor.*;
*Nucleotide sequence of the bovine vitamin D3 receptor.*;
*J. Dairy Sci. 79:1313-1315(1996).
*I'FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLL
*THE EXPRESSION OF HORMONE SENSITIVE GENES.
*I'SUBCELLULAR LOCATION: NUCLEAR HORMONE NOT THE SUBCELLULAR LOCATION: NUCLEAR HORMONE RECEPTORS FAMILY
*I'DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING NOTATION ADD A C-TERMINAL STEROID-BINDING DOMAIN AND A C-TERMINAL STEROID
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Bos taurus (Bovine).
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y; p03372; 1HCQ.
RRPRO; IPR000324; -.
RRPRO; IPR000536; -.
RRPRO; IPR001628; -.
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                                 RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA
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RLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEEALKDSLRPK-LSEEQQRIIAILLDA
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C4-TYPE.
C4-TYPE.
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Pred. No. 4.1e-56;
7; Mismatches 143
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E9E24926CE38CB7D
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RESULT 10
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MEDILINE-88217887; PubMed-2835767;

Baker A.R., McDonnell D.P., Hughes M., Crisp T.M., Ma
Baker A.R., McDonnell D.P., Shine J., O'Malley B.W.;

"Cloning and expression of full-length cDNA encoding"
                                                                                                             TISSUE-PERIPHERAL BLOOD;
MEDLLINE-91210272; PubMed-1B50412;
Yu X.-P., Mocharla H., Hustmyer F.G., Manolagas S.C.;
"Vitamin D receptor expression in human lymphocytes.:
requirements and characterization by western blots ansequencing.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LENS EPITHELIUM;
Rae J.L., Shepard A.R.;
Submitted (SEP-1997) to
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MEDLINE-92379083; PubMed=1324736;

GOLO H., Chen K.S., Prahl J.M., Deluca H.F.;

GOLO H., Chen K.S., Prahl J.M., Deluca H.F.;

"A single receptor identical with that from intestine/T47D mediates the action of 1,25-dihydroxyvitamin D-3 in HL-60 c Biochim. Biophys. Acta 1132:103-108(1992).
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Eukaryota; Metażoa; Chordata;
Mammalia; Eutheria; Primates;
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VARIANTS ASP-33' AND MEDLINE-89072761; Pu
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Endocrinol, 11:11
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S.; Inoue Y., Morita K., Takeda E., Pike J.W.;
ral organization of the human vitamin D receptor.
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                                                                                      266:7588-7595(1991)
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MEDIINE-97120600; PubMed-8961271; Whitfield G.K., Selznick S.H., Haussler C.A., Hsleh J.-C. Galligan M.A., Jurutka P.W., Thompson P.D., Lee S.M., Ze Haussler M.R.; Thompson P.D., Lee S.M., Ze Haussler M.R.; Witamin D receptors from patients with resistance to 1, dilydroxyvitamin D(3): point mutations confer reduced tr in response to ligand and impaired interaction with the receptor heterodimeric partner."; Mol. Endocrinol. 10:1617-1631(1996).
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Mol.
[10]
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"A new point mutation in the deoxyribonucleic acid-binding
the vitamin D receptor in a kindred with hereditary
1,25-dihydroxyvitamin D-resistant rickets.";
J. Clin. Endocrinol. Metab. 76:509-512(1993).
                                                                                                                  VARIANTS SER-314 / MEDLINE=97120600; Whitfield G.K., Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malloy P.J., Weisman Y., Feldman D.
"Hereditary I alpha, 25-dihydroxyvitamin D-
from a mutation in the vitamin D receptor
acid-binding domain.";
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"A unique point mutation in the human vitamin D receptor chromosomal gene confers hereditary resistance to 1,25-dihydroxyvitamin D3.";
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"A unique mutation in the vitamin D receptor gene in three patients with vitamin D-dependent rickets type II: utility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Point mutations in the human hypocalcemic rickets."; Science 242:1702-1705(1988).
                                                                                                                                                                                                           vitamin D receptor
rickets.";
                                                                                                                                                                                                                                           "A novel mutation in the
                                                                                                                                                                                                                                                                                                                                                structures."
                                                                                                                                                                                                                                                                                                                                                               "Two mutations causing vitamin D basis of steroid hormone receptor
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MEDLINE-91125370; PubMed-2177843;
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MEDLINE-93163233; PubMed-8381803;
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Feldman D., O'Malley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tjansson K., Rut A.R., Hewison M., O'Riordan J.L.H., Hughes M.R.; mutations in the hormone binding domain of the vitamin D ptor cause tissue resistance to 1,25 dihydroxyvitamin D3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            confers hereditary resistance Endocrinol. 4:623-631(1990).
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D'Malley B.W.;
                                                                                                                                                         AND CYS-391
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                                                                                                                                                                                                                       P.J., Sakati N., Al-Ashwal A., Feldman D.; in the deoxyribonucleic acid-binding domain of the causes hereditary 1,25-dihydroxyvitamin D-resistant
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r DNA-binding
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ee S.M., Zerw
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transactivation
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of single-
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     INTERPRO: IPR000324; -.
INTERPRO: IPR000536; -.
INTERPRO: IPR001628; -.
PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS: PR00047; STROIDEINGER.
PRINTS: PR00350; VITAMINDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the vitamin D receptor that results in decreased affinity for hormone and cellular hyporesponsiveness.";

J. Clin. Invest. 99:297-304(1997).

-I- FUNCTION: VDR MEDIANTES THE ACTION OF VITAMIN D3 BY CONTROLLING THE EXPRESSION OF HORMONE SENSITIVE GENES.

-I- SUBCELLULAR LOCATION: NUCLEAR.

-I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

-I- DOMAIN BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

-I- DISEASE: DEFECTS IN VDR ARE THE CAUSE OF TYPE IIA RICKETS (ALSO KNOWN AS HYPOCALCEMIC VITAMIN D-RESISTANT RICKETS (HYDRR)). HYDRR IS MOST FREQUENTLY AN AUTOSOMAL RECESSIVE DISCREES CHARACTERIZED BY SEVERE RICKETS, HYPOCALCEMIA AND SECONDARY HYPERPARATHYROIDISM.

-I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                         DNA_BIND
ZN_FING
ZN_FING
                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A28200; A28200.
PIR; S24174; S24174.
HSSP; P03372; 1HCQ.
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EMBL;
EMBL;
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EMBL;
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                                                     VARIANT
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                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                       VARIANT
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AB002166;
AB002167;
M65208; AA
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X67482; CAA47824.1;
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24 89 C4
24 44 C4
60 84 C4
90 191 H1
192 427 L1
193 33 33 G
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G -> D (IN RICKETS).
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F -> I (IN RICKETS).
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K -> E (IN RICKETS).
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G -> D (IN RICKETS).
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Nuclear

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RESULT
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Best Local Sin
Matches 174;
 use by modified
                                                                                                               MEDINE-94158927; PubMed-8114692;
MEDINE-94158927; PubMed-8114692;
Baes M., Gullck T., Choi H.S., Martinoli M.G., Simha D., Moore D.:
Baes M., Gullck T., Choi H.S., Martinole receptor superfamily
"A new orphan member of the nuclear hormone receptor superfamily
interacts with a subset of retinoic acid response elements.";
MOI. Cell. Biol. 14:1544-1552(1994).
-1- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE
ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTO
BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES.
-1- SUBGULT: HETERODIMER OF NRII3 AND RAR.
-1- SUBGULT: HETERODIMER OF NRII3 AND RAR.
-1- SUBGULTULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
0RPHAN NUCLEAR RECEPTOR NRII3 (CONSTITUTIVE ANDROSTANE RECEPTOR) (CAR)
(ORPHAN NUCLEAR RECEPTOR MB67).
                                                    between
                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q14994;
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                                                                                                           NR1 SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSY----CLEDTAGGFQQLLLE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDSSSFSNLDLSEEDSD-----DPSVTLELSQLSMLPHLADLVSYSIQKVIGFAKMIPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICGYCGDRATGFHENAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHKTYDPTYSDFCQFRPPVRVNDGGGSHPSRPNSRHTPS--FSGDSSSSSCSDHCITSSDM
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non-profit
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42.2%;
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Pred. No. 4.2e-56;
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/FTId=VAR_004661.
R -> Q (IN RICKETS).
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Best Local Similarity
Matches 164; Conserv
                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                 NRI3_RAT STANDARD: PRT; 358 AA. 09QUS1; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) 0RPHAN NUCLEAR RECEPTOR NRII3 (CONSTITUTIVE A
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PFAM; PF00105; zf-C4; 1.

PRINTS; PR00047; STROIDFINGER.

PRINTS; PR0035C; VITAMINDR.

PRINTS; PR005546; THYROIDHORMS.

PROSITE; PR0003F, NUCLEAR_RECEPTOR; 1.

Receptor; Transcription regulation; DNA-binding; Nuclear protein;

Zinc-finger; Activator.
STRAIN-WISTAR KYOTO, AND FISCHER; Yoshinari K., Sueyoshi T., Moore I
                                                                                                                                                                                                                      (CAR)
                                                       SEQUENCE FROM N;A.
                                                                                                                                                                                          NR1I3 OR CAR.
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INTERPRO; IPROCO536; -.
INTERPRO; IPROC1628; -.
INTERPRO; IPROC1728; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELCOLRENTVENAETGTWECGRLSYCLEDTAG-GFQQLLLEPMLKFHYMLKKLQLHEEE
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     Moore R., Negishi M.;
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Pred. No.
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C4-TYPE.
C4-TYPE.
                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                              TISSUE-LIVER;
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Best Local
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INTERPRO; IPRO01528; -.
INTERPRO; IPRO01728; -.
INTERPRO; IPRO01728; -.
INTERPRO; IPRO01728; -.
INTERPO; IPRO01728; -.
PEAM; PF00104; bormone_rec; l.
PFAM; PF00105; zf-C4; l.
PFAM; PF00105; zf-C4; l.
PFAMTS; PR00036; VITAMINDR.
PRINTS; PR00350; VITAMINDR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00398; STRDHORMONER.
PROSITE; PR00391; NUCLEAR_RECEPTOR: 1
Receptor; Transcription regulation; Di
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ZN_FING
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321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEEYGPRNCVVCGDRATGYHFHALTCEGCKGFFRRTVSKTIGPICPF-AGRCEVSKAQRR
                                                                                                                                                                                                                                                         ISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAG-GFQQLLLEPMLKFHYMLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCPACRLQKCLNVGMRKDMILSAEALALRRARQARRRAQKASLQ-----LSQQQKELIQ 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVGGPOICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRR
                                       KIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQEL
KLMGLLAELRSINSAYSYEIHRIQGLSAM-MPLLGEI
                                                                                                                                                                     KLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFL 391
                                                                                                                                                                                                                        ISLLKGAAVEILHISLNTTFCLQTQNFFCGPLCYKMEDAVHYGFQYEFLELIIHFHKTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLGAHTRHVGPMFDQFVQFRPPAYLFSH-HRPFQPLAP---
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                                                                                             ALMAAMALFSPDRPGVTQREEIDQLQEEVALILNNHIMEQQSRLQSRFLYA
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                                                                                                                                                                                                                                                                                                                                              ----VLPLLTHFADINTFMVQQIIKFTKDLPLFRSLTMEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 729; DB 1; Length 358; Pred. No. 2.2e-51; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13691F49CAD8F1ED CRC64;

    DNA-binding; Nuclear protein;

   356
                                                         428
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NRIS_MOUSE STANDARD; PRT; 358 AA.

AC 035627; 035628;
DT 15-UUL-1999 (Rel. 38, Created)
DT 15-UUL-1999 (Rel. 38, Last sequence update)
DT 01-000 (Rel. 40, Last annotation update)
DT 01-000T-2000 (Rel. 40, Last annotation update)
DT 01-000T-2000 (Rel. 40, Last annotation update)
DT 01-000T-2000 (Rel. 40, Last annotation update)
DT 01-00T-2000 (Rel. 40, Last annotation update)
DT
                                                                                          INTERPRO; IPNOUT 18; ...

A INTERPRO; IPROUNT 18; ...

R PEAM; PEO0104; 'hormone_rec; 1.

R PEAM; PEO0105; Zf-C4; 1.

DR PRINTS; PRO0047; STROIDFINGER.

DR PRINTS; PRO0350; VITAMINDR.

DR PRINTS; PRO0398; STRNDEORMONER.

DR PRINTS; PRO0531; NUCLEAR_RECEPTOR; 1.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

C4-TYPE ZINC FINGERS (TWO).

---FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hormone receptor CAR.";
J. Biol. Chem. 272:3365-23571(1997).

J. Biol. Chem. 272:3365-23571(1997).

FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE ELEMENTS TRAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES.

-I- SUBUNIT: HETERODIMER OF NRII3 AND RXR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Differential transactivation by two isoforms of the orphan nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAR1 (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING. CAR2 DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PREDOMINANTLY EXPRESSED IN LIVER. TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                  DRPGVT -> GFCMQS (IN ISOFORM CAR2).
MISSING (IN ISOFORM CAR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                       4F07730FF78CADBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simha D., Lee Y.-K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                          CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus.
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Q

31 ADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKT 90

Query Match
Best Local Similarity
Matches 157; Conserv

Conservative

31.7%;

%; Score 725; DB %; Pred. No. 4.6e 64; Mismatches

DB 1; .6e-51;

Indels

54;

Gaps

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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                 Zinc-finger.
                                                 Receptor; Transcription
                                                             PRINTS; PRO0047; STROIDFINGER.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                 PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
                                                                                                                                                                    EMBL; AF085745; AAD16050.1; -. HSSP; P20393; 1A6Y.
                                                                                                                                                                                                                                                                                                                                                                                   Chen Y.E., Horiuchi M., Dzau V.J.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH RXR
SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN
ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES
1 SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Vammalia, Futheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OXYSTEROLS RECEPTOR LXR-ALPHA (LIVER X RECEPTOR ALPHA) (NUCLEAR ORPHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR LXR-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRH3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 YAKLMGLLADLRSINNAYSYELQRLEELSAM-TPLLGEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 FLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQEL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 VQILLGAHTRHVGPLFDQFVQFKPPAYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
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                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                          NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTA-GGFQQLLLEPMLKFHYM 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQISLLKGAAVEILHISLNTTFCLQTENFFCGPLCYKMEDAVHAGFQYEFLESILHFHKN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLK 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKGLHLQEPEYYLMAATALFSPDRPGYTQREEIDQLQEEMALILNNHIMEQQSRLQSRFL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRHCPACRLQKCLNVGMRKDMILSAEALALRRARQAQRRAEKASLQ-----LNQQQKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRQCQACRIRKCIESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPIGVQGITEEQRMM 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASEEEYGPRNCVVCGDRATGYHFHALTCEGCKGFFRRTVSKTIGPICPF-AGRCEVSKAQ 69
                                                                                                                                  1PR000536; -.
IPR0001628; -.
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96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
116
                                          regulation; DNA-binding; Nuclear protein;
C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                           MEDLINE-95011628; PubMed-7926814;
Shinar D.M., Endo N., Rutledge S.J., Vogel R., Rodan G.A., Schmidt A.;
Shinar D.M., Endo N., Rutledge S.J., Vogel R., Rodan G.A., Schmidt A.;
"NER, a new member of the gene family encoding the human steroid
hormone nuclear receptor.";
Gene 147:273-276(1994).
-!- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
OLIGONOCLEGIDED DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
SEQUENCE 5'-AGGICA-3' AND 4-NT SPACING (DR-4).
-!- SUBURIT: FORMS A HETERODIMER WITH RXR.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIBCLELLULAR LOCATION: NUCLEAR HORMONE RECEPTORS FAMILY.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 34, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
OXYSTEROLS RECEPTOR LXR-BETA (LIVER X RECEPTOR BETA) (NUCLEAR ORPHAN
RECEPTOR LXR-BETA) (UBIQUITOUSLY-EXPRESSED NUCLEAR RECEPTOR) (NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRH2_HU
P55055;
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR NER).
NR1H2 OR LXRB OR UNR OR NER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 LMQELFGI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 VSVQEIVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSRRYNPGSESITF-LKDFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 -HSGGHCPMITYMRRKCQECRLRKCRQAGMREECVLSEEQIRLKK--LKRQEEEQAQATS
                                                                                                                                                                                                                                                                                         SSUE-OSTEOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 EPTELRPQKRKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGARYVC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 EDTESVPGKESVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                  NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLSEIWDV 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHTYVEALHAYVSINHPHDP--LMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYYLMQAISLFSPDRPGVLQHRVVDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFN--AETGTWECGRLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSPRVSSPPCVLPQLSPEQLGMIEKLVAAQQQCNRRSFS-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129;
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445 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 C
50417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.8%; Score 498.5; DB 1; 30.1%; Pred. No. 9.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1A426DF38D935731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.7%; Score 498; DB 1; Length 461; Best Local Similarity 29.0%; Pred. No. 1.1e-32; Matches 126; Conservative 86; Mismatches 125; Indels 98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRODO47; STROIDFINGER.
PROSITE; PRO0031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U07132; AAA61783.1; -.
HSSP; P03372; 1HCQ.
MIM; 600380; -.
INTERPRO; IPR001638; -.
INTERPRO; IPR001638; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00104; hormone_rec; 1. PFAM; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                               184 LPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHM 243
                                                                                                                                                                                                                                                                                                                                201 SPGGSEAGSQGSGEGEGYQLTAAQELMIQQLVAAQLQCNKRSFS----------- 244
                                                                                                                                                                                                                                                                                                                                                             143 ------LTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCE 183
                                                                                                                                                                                                                                                                                                                                                                                             272 TELAIISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECIT 328
                                                                                                                                                                                                                            244 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC-- 301
                                                             389 PGRVEALQQPYVEALLSYTRIKRPQDQLR--FPRMLMKLVSLRTLSSVHSEQVFALRLQD 446
                                                                                              359 HRYVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQD 416
                                                                                                                             329 FLKDFTYSKDDFHRAGLQVEFINFIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQE 388
                                                                                                                                                               302 -- GRLSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQ 358
447 -- KKLPPLLSEIWDV 459
                               417 IHPFATPLMQELFGI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 GPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 C. 107 C. 149 C. 15176 P. 176 P. 196 P. 196 P. 151102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
C4-TYPE.
LICAND-BINDING (POTENTIAL).
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68CE3D9F9BC5C0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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Search completed: February 18, 2001, 13:43:38 Job time: 5858 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2001, 13:03:51; Search time 57.29 Seconds (without alignments) 514.381 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-143-828-2 2290 1 MEVRPKESWNHADFVHCEDT......ODIHPFATPLMQELFGTTGS 434

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

195891 segs, 67900655 residues

Searched:

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

1455175 first 45 summaries

Database : PIR_66;

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.

SUMMARIES

24) A	4 6) i	٥ ا	2	24	23	22	12) \ \ \) L	· -	; <u>-</u>	; t	: 5	1	1.5		; ;	. C	, ,	a	• ~	ıσ	, U	4.	٠ لـ	N	, <u>,</u>	NO.	Result	
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A41055	A43786	1210AP	AUGUUA	2000	30000	A31820	A40377	D36067	TVHUAR	C36067	I51165	S58211	TVCHTB	149018	A56918	159354	149021	138975	A56043	JC4014	A56197	S24174	A28200	JC7230	PC4019	A31761	150451	JC7229	S41497	Į.		
	retinoic acid rece	thyroid hormone re			TICTIONE	hormone	hormone	hormone	hormone	oid hormone r	gene c-erbA-beta p			retinoid X recepto	farnesoid x-activa	orphan nuclear rec	retinoid X recepto	nuclear orphan rec	steroid hormone re	steroid hormone-nu	nuclear hormone re	vitamin D receptor	vitamin D receptor	U	ם סי	1,25-dihydroxyvita	U	D recept	oid hormone			

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416	417.5	418	418	421.5	421.5	421.5	422	423.0	,	, () . (» л	427	427	42/.5	3 1	428	428	
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etinoic acid rece	nuclear receptor	hyroid hormone re	hyroid hormone re	hyroid hormone re	old r	acid	retinoic acid rece	acid	retinoic acid rece	chyroid hormone re	errnore acto rece		retinoic acid rece	nuclear receptor I	rectnote acto tece	-	retinoic acid rece	

ALIGNMENTS

thyroid hormone receptor homolog - African clawed frog (;Species: Xenopus laevis (African clawed frog) (;Species: Xenopus laevis (African clawed frog) (;Date: 20-May-1994 #sequence_revision 26-May-1995 #text_change 20-Sep-1999 (;Accession: S41497; S38486 R;Smith, D.P.; Mason, C.S.; Jones, E.A.; Old, R.W. Nucleic Acids Res. 22, 66-71, 1994 A;Title: A novel nuclear receptor superfamily member in Xenopus that associates with A;Reference number: S41497; MUID:94173664 A;Reference number: S41497; MUID:94173664 A;Accession: S41497 A;Status: preliminary; nucleic acid sequence not shown A;Accession: First Symiler (Sano) A;Residues: 1-386 <smi) 1-386="" <erba="" <smi)="" a;cross-references:="" a;residues:="" c;reywords:="" domain:="" embl:x75163;="" erba="" f;35-303="" finger="" homology="" nid:9410517;="" pid:9410518="" pidn:caa53006.1;="" protein="" transforming="" zinc=""></smi)>

9

Que Bes oy	ry M t Loo ches 18 14 78 78 73 74 137 137 137 137 137 133 197 172 2257	Query Match 43.3% Score 991.5; DB 2; Length 386; Best Local Similarity 49:0%; Pred. No. 6.4e-70; Matches 204; Conservative 59; Mismatches 104; Indels 49; Gaps 18 EDTESVPGKPSVNADEEVGGPOICRVCGDKATGYHENAMTCEGCKGFFRRAMKRNARLRC 77
γQ	78	PFRKGACEITRKTRROCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRK-KSERTGTQ 136
В	74	PF-QNSCVINKSNRRHCQACREKKCLDIGMRKELIMSDAAVEQRRALIKRKHKLTKLPPT 132
Qy	137	PLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEA 196
8	133	PPGA-SLTPEQQHELTQLVGAHTKTEDFNETFSKNERPIR 171
ОУ	197	AKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIIS 256
윩	172	RSSDPTQEPQATSSEAFLMLPHISDLVTYMIKGIIS 207
Qy	257	FAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT-AGGF 315
В	208	FAKMLPYFKSLDIEDQIALLKGSVAEVSVIRFNTVFNSDINTWECGPFTYDTEDMFLAGF 267
νo	316	QQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKS 375
ઠ	268	RQLFLEPLVRIHRMARKLNIQSEEYAMMAALSIFASDRPGVCDWEKIQKIQEHIALTIKD 327
Qy	376	YIECNR-PQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFG 430
D.	328	328 FIDSQRPPSPQNRLLYPKIMECLTELRTVNDIHSKQLLEIWDIQPDATPLMREVFG 383

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A;Gene: vdr-a
C;Superfamily: unassigned
C;Keywords: bone; calcium
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C;Superfamily: unassigned erbA-related C;Keywords: zinc finger
                                                                                                                                                              vitamin D receptor isoform A - Japanese quail
Q:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C:Accession: I50451
R:Elaroussi, M.A.; Prahl, J.M.; Deluca, H.F.
R:Elaroussi, M.A.; Prahl, J.M.; Deluca, H.F.
R:Coc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994
A;Title: The avian vitamin D receptors; primary structures and t
A;Reference number: I50451; MUID:95062315
A;Accession: I50451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: DDBJ:AB037673
A; Experimental source: intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 270, 40-45, 2000
A; Title: Identification of cDNAs encoding two subtypes of vitamin D receptor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
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                                                 A; Cross-references: EMBL: U12641; NID: 9595500; PIDN: AAA56725.1; PID: 9595501
                                                                                    A; Molecule type: mRNA
A; Residues: 1-448 <ELA>
                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local S
Matches 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :Comment: This receptor is an important factor in calcium homeostasis and bone formati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 PGFRDLTAEDQIALLKSSAIEIIMLRSNQSFSLEDMSWSCGGPDFKYCINDVTKAGHTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VGPDEFDRNAPRICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKASFTCPF-NGSCTIT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 VNADE-EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEIT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNRPQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQDIHPF-ATPLMQELFG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLCSLKY---SLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSSGCELPESLQAPSREEAAKWSQVRK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDNRRHCQACRLKRCIDIGMMKEFILTDEEVQREKEMILKRKEEEAAREAMRPR-LNEEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLEPLYKFQVGLKKLNLHEEEHVLLMGICLLSPDRPGVQDHARVEQLQDRLPEALQAYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECG--RLSYCLED-TAGGFQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SV-DTKMNFSNLLMMYQDGA----SSPDSSEENTKLSMLPHLADLVSYSIQKVIGFAKMI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARMISSIVEAHHKTYDASYSDFSRFRPPVREGPVTRSASRAASIHSISDASSDSFNHSPE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN--HPGGRLLYAKMIQKLADLRSLNEEHSKQYRSLSFQPEHSMQLTPLVLEVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erbA-related proteins; erbA transforming protein homology transport; DNA binding; hormone receptor; intestine; vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 817; DB 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                proteins; erbA transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 420
                                                                                                                                                                                                                                 structures and their origins.
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F;42-362/Domain: erbA transforming protein homology <ERBA>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999
C;Accession: A31761; A31367
C;Accession: A31761; A31367
R;Burmester, J.K.; Wiese, R.J.; Maeda, N.; DeLuca, H.F.
Proc. Natl. Acad. Sci. U.S.A. 85, 9499-9502, 1988
A;Title: Structure and regulation of the rat 1,25-dihydroxyvitamin D-3 receptor.
A;Reference number: A31761; MUID:89071726
A;Accession: A31761; MUID:89071726
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                                                                                                             C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology c;Keywords: DNA binding; transcription regulation; zinc finger F;22-337/Domain: erbA transforming protein homology <ERBA> F;24-44/Region: zinc finger F;60-84/Region: zinc finger
                                                                                                                                                                                                                                                                                     R;Burmester, J.K.; Maeda, N.; DeLuca, H.F.
Proc. Natl. Acad. Sci. U.S.A. 85, 1005-1009, 1988
A;Title: Isolation and expression of rat 1,25-dihydroxyvitamin D-3
A;Reference number: A31367; MUID:88124963
A;Accession: A31367
                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 'R', 58-423 <BU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-423 <BUR>
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                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CESQELQSSDMETPAVGTPEFDRNVPRICGVCGDRATGFHFNAMTCEGCKGFFRRSMKRK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEDTE---SVEGKPSVNADE-EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALKESLKPK-LSEEQQKVINILLEAHHKTFDTTYSDFNKFRPPVRSKFSSSTATHSSSVV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMETICPF-SGDCKITKDNRRHCQACRLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSER 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLPHLADLVSYSIQKVIGFAKMIPGFRDLTAEDQIALLKSSAIEVIMLRSNQSFIMEDMS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTCGSNDFKYKVSDVTQAGHSMDLLEPLVKFQVGLKKLNLHEEEHVLLMAICILSPDRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQDFSSEDSNDVFGSDAFGAFPEPMEPQMFSNLDLSEESDESPSMNIELPH-----LP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQDTSLVESIQDRLSDTLQTY TRCRHPPPGSRLLYAKMIQKLADLRSLNEEHSKQYRCLS
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40.9%; Pred. No. 4.2e-56;
                    35.0%;
                         Score 801; DB 2; Pred. No. 5.3e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                   Length 423;
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38 PQICRVCGDKI.TGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 97

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A; Molecule type: mRNA
A; Residues: 1-422 <KRM>
A; Residues: 1-422 <KRM>
A; Residues: 1-422 <KRM>
A; Cross-references: DDBJ.D31969; NID:g699618; PIDN:BAA06737.1; PID:d1007311; PID:g69961:
A; Cross-references: DDBJ.D31969; NID:g699619; PIDN:BAA06737.1; PID:d1007311; PID:g699619;
C; Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C; Keywords: DNA binding; finc finger
F; 24-336/Domain: DNA binding #status predicted <BIN>
F; 24-89/Domain: DNA binding #status predicted
F; 191-422/Region: vitamin D binding #status predicted
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C;Accession: PC4019
R;Kamei, Y.; Kawada, T.; Fukuwatari, T.; Ono, T.; Kato, S.; Sugimoto, R;Kamei, Y.; Kawada, T.; Fukuwatari, T.; Ono, T.; Kato, S.; Sugimoto, R;Kamei, Y.; Kawada, T.; Fukuwatari, T.; Ono, T.; Kato, S.; Sugimoto, R;Kamei, Y.; Sugimoto, R;Ka
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A;Accession: PC4019
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                                                 IPGFRDLTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDITDVSRAGHTL 302
                                                                                                                 ISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT---AGGFQQ 317
                                                                                                                                                                                                                                                                                                                         HHKTYDPTYADFRDFRPPIRADVSTGSYSPRPTLSFSGDSSSNSDLYTPSLDMMEPASFS
                                                                                                                                                                                                                                                                                                                                                                                         QMKTFDTTFSHFKNFRLP--GVLSSGCELP------ESLQAPSRE--EAAKWS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQQHIIAILLDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQAC 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQDYKYDVTDVSKAGHTLELIEPL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHKTYDPTYADFRDFRPPVRMDGSTGSYSPR----PTLSFSGNSSSSSSDLYTTSLDMME 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QMKTFDTTFSHFKNFRLPGVL--SSGCELPESLQAPSREENAKWSQVRKDLCSLKV---- 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.6%; Score 792.5; DB: 41.8%; Pred. No. 2.4e-54
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C;Accession: JC7230
C;Accession: JC7230
R;Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T.
Biochem. Biophys. Res. Commun. 270, 40-45, 2000
Biochem. Biophys. Res. Commun. 270, 40-45, 2000
A;Title: Identification of cDNAs encoding two subtypes of vitamin
A;Reference number: JC7229
vitamin D receptor - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1989 *sequence_revision 19-May-1989 *text_change 20-Sep-1999
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C;Comment: This receptor is an important factor in calcium homeostasis and bone forma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vitamin D receptor subtype b - Paralichthys olivaceus C; Species: Paralichthys olivaceus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-425 <SUZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 PSREEAAKWSQVRKDLCSLKVS----LQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 GTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSSGCELPESLQA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 KGACETTRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKK-----SERT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 SVPGKPSVNADE-EVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TVVSTSSLASDEFDRNMPRICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKATFTCPF- 62
                                                                                                                                                                                                                                                                                                                     ATPLMQELFG 430
                                                                                                                                                                                                                                                                                                                                                                                     ALQDRLSETLQAYIQLH--HPGGRLLYAKMIQKLADLRSLNEEHSKQYRSLSFRPEHSMQ
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                                                                                                                                                                                                                                                  LTPLVLEVSG 421
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C;Accession: S24174
R;Goto, H.; Chen, K.; Prahl, J.M.; DeLuca, H.F.
Biochim. Biophys. Acta 1132, 103-108, 1992
A;Title: A single receptor identical with that from intestine/T47D cells mediates A;Reference number: S24174; MUID:92379083
A;Accession: S24174
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A;Title: Vitamin D receptor expression in human lymphocytes. A;Reference number: I55353; MUID:91210272
A;Accession: I55353
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R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, Proc. Natl. Acad. Sci. U.S.A. 85, 3294-3298, 1988
A;Title: Cloning and expression of full-length cDNA encoding human vitamin D receptor. A;Reference number: A28200; MUID:88217887
A;Accession: A28200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 12q12-12q14
C;Superfamily: unassigned erbA-related proteins; erbA transforming C;Keywords: DNA binding; transcription regulation; zinc finger F;22-341/Domain: erbA transforming protein homology <ERBA> F;24-44/Region: zinc finger F;60-84/Region: zinc finger
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A; Cross-references: GDB: 120487; OMIM: 601769; OMIM: 277440
                                                                                                                                                        C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                       vitamin D receptor - rat
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A; Residues: 24-90 < RES>
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A; Residues: 1-427 <BAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDSSSFSNLDLSEEDSD-----DPSVTLELSQLSMLPHLADLVSYSIQKVIGFAKMIPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWTCGNQDYKYRVSDVTKAGHSLELIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHKTYDPTYSDFCQFRPPVRVNDGGGSHPSRPNSRHTPS--FSGDSSSSCSDHCITSSDM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 157
                                                                                                                                                                                                                                                                                                                                      PPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLVLEVFG
                                                                                                                                                                                                                                                                                                                                                                                     PQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQ-DIHPFATPLMQELFG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                       PLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSY - - - CLEDTAGGFQQLLLE
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nilarity 42.2%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 789; DB 2;
Pred. No. 4.7e-54;
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A; Molecule type: mRNA
A; Residues: 1-427 <GOTS
A; Residues: 1-427 <GOTS
C; Superfamily: unassigned erbA-related proteins; erbA transforming
C; Keywords: DNA binding; transcription regulation; zinc finger
F; 22-341/Domain: erbA transforming protein homology <ERBA>
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Best Local
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                                                        372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
9
                                                    PPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLVLEVFG
                                                                          PQPAHRFLFLKIMAMLTELRSINAQHTQ--RLLRIQ-DIHPFATPLMQELFG 430
                                                                                                                              PLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRH
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                                                                                                                                                    PMLKFHYMLKKLQLHEEEYYLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNR
                                                                                                                                                                                                       RDLTSEDQIVLLKSSAIEVIMLRSNESFIMDDMSWTCGNQDYKYRVSDVTKAGHSLELIE
                                                                                                                                                                                                                                          RDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSY---CLEDTAGGFQQLLLE
                                                                                                                                                                                                                                                                                   MDSSSFSNLDLSEEDSD-----DPSVTLELSQLSMLPHLADLVSYSIQKVIGFAKMIPGF
                                                                                                                                                                                                                                                                                                                    ---SLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYF 264
                                                                                                                                                                                                                                                                                                                                                       HHKTYDPTYSDFCQFRPPVRVNDGGGSHPSRPNSRHTPS--FSGDSSSSCSDHCITSSDM 196
                                                                                                                                                                                                                                                                                                                                                                                                                               RLKRCVDIGM/KEFILTDEEVQRKREMILKRKEEEALKDSLRPK-LSEEQQRIIAILLDA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
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Pred. No. 4.7e-54;
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C;Accession: A56197
R;Baes, M.; Gulick, T.; Choi, H.S.; Martinoli, M.G.; Simha, D.; Moore, D.D. Mol. Cell. Biol. 14, 1544-1552, 1994
A;Title: A new orphan member of the nuclear hormone receptor superfamily that A;Reference number: A56197; MUID:94158827
A;Accession: A56197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuclear hormone receptor MB67 - human
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 20-Sep-1999
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C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
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A; Residues: 1-348 <BAE>
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                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: unassigned erbA-related Reywords: zinc finger
                                                                                                                                                                                                                                                         Matches 164;
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Best Local Similarity
                                                                                                  101
     161 TFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDG 220
                                                 70 KCLDAGMRKDMILSAEALALRRAKQAQRRAQQTPVQ-----LSKEQEELIRTLLGAHTR 123
                                                                                                                                                                                                     41 CRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLR 100
                                                                             KCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTOPLGVQGLTEEQRMMIRELMDAQMK 160
                                                                                                                                                      CVVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPF-AGSCEVSKTQRRHCPACRLQ 69
                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.
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Db 245DQPKVTPWP	126; CONSETVALIVE 8; 136; CONSETVALIVE 8; 17 GPQICRYCGDKATGYHENVMTCEC 18 ::	A; Molecule type: mRNA A; Residues: 1-461 <shi> A; Cross-references: GB:U07132; NID:g641961; PIDN:AAA61783.1; PID:g641962 A; Cross-references: GB:U07132; NID:g641961; PIDN:AAA61783.1; PID:g641962 A; Experimental source: osteosarcoma cells SAOS-2/B10 C; Genetics: A; Experimental source: osteosarcoma cells SAOS-2/B10 C; Genetics: A; Cross references: GDB:389570; OMIM:600380 A; Map position: 19q13.3-19q13.3 C; Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C; Keywords: steroid hormone receptor F; 85-381/Domain: erbA transforming protein homology <erba> F; 87-154/Domain: DNA binding #status predicted <bin> Ouery Match 21.7%; Score 498; DB 2; Length 461;</bin></erba></shi>	Qy 400 LRSINAQHTQRLLRIQDIHPFATPLMQEL 428	Db 124 HMGTMFEQFFVGFRPAHLFIHHQ-PLPTLAP
Oy 424 LMQELFGI 431 : ::: Db 436 LLSEIWDV 443 RESULT 12 138975 1000 septor LXR-alpha - human C:Species: Homo sapiens (man) C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 20-Sep-1999 C:Accession: 138975 ::	QY 189 QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 248 Db 229DRLRVTPW-PIAPD	Query Match Query Match Query Match Query Match Best Local Similarity 30.1%; Score 496.5; DB 2; Length 445; Best Local Similarity 30.1% Pred. No. 3.3e-31; Matches 129; Conservative 84; Mismatches 144; Indels 71; Gaps 13; Qy 18 EDTESVPGKPSVNADEEVGGPOICRVCGDKANTGYIFNVNTCEGCKGFFRRAMKRNARLRC 77	C:Accession: A56043 R;Apfel, R:, Benbrock, D.; Lernhardt, E.; Ortiz, M.A.; Salbert, G.; Pfahl, M. Mol. Cell. Biol. 14, 7025-7035, 1994 A:Title: A novel orthan receptor specific for a subset of thyroid hormone-responsive A;Reference number: A56043; MUID:95021230 A;Accession: A56043 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-445 < App. A;Cross-references: GB:U11685; NID:g555751; PIDN:AAA53633.1; PID:g555752 A;Cross-references: GB:U11685; NID:g555751; PIDN:AAA53633.1; PID:g555752 A;Mote: authors translated the codon GAG for residue 73 as Ser C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Keywords: steroid hormone receptor; zinc finger F;94-365/Domain: erbA transforming protein homology < ERBA>	Qy 359 HRVVDQLQECFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQD 416

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R:Willy, P.J.; Umesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J. Genes Dev. 9, 1033-1045, 1995
A:Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway.
A:Reference number: I38975; MUID:95262897
A:Accession: I38975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMEL:U22662; NID:g726512; PIDN:AAAB5856.1; PID:g726513
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: zinc finger
F;96-367/Domain: erbA transforming protein homology <ERBA>
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A; Residues: 1-447 < RES>
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                                                                                                                                                                                                                                                                                                                         retinoid X receptor interacting protein No.15 - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Unl-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999 C;Accession: I49021
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Mol. Endocrinol. 9, 72-85, 1995
A;Title: Isolation of proteins that interact specifically A;Reference number: A57664; MUID:95280959
A;Accession: I49021
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A;Gene: RIP15
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Keywords: zinc finger
C;Keywords: zinc finger
F;76-366/Domain: erbA transforming protein homology <ERBA>
                                                                                            A;Cross-references: EMBL:U09419; NID:g691713; PIDN:AAC52164.1; PID:g691714 C;Genetics:
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A; Residues: 1-446 < RES>
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Best Local S
Matches 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMST 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPTEIRPQKRKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFRRSVIKGAHYIC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEDTA-GGFQQLLLEPMLKFHYMLKKLQLHEEEYYLMQAISLFSPDRPGVLQHRVVDQL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPPRRSSPPQILPQLSPEQLGMIEKLVAAQQQCNRRSFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHTYVEALHAYVSIHHPH--DRLMFPRMLMKLVSLRTLSSVHSEQVFALRLQD--KKLPP 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFN--AETGTWECGRLSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLSEIWDV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFATP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NREDFAKAGLQVEFINPIFEFSRAMNELQLNDAEFALLIAISIFSADRPNVQDQLQVERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 491.5;
Pred. No. 8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                 the retinoid X receptor:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Teboul, M.; Enmark, E.; Li, Q.; Wikstrom, A.C.; Pelto-Huikko, M.; Gustafsson, J.A. proc. Natl. Acad. Sci. U.S.A. 92, 2096-2100, 1995
A;Title: OR-1, a member of the nuclear receptor superfamily that interacts with the A;Reference number: I59354; MUID:95199298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                      A;Experimental source: Sprague-Dawley, hepatic R;Song, C.; Kokontis, J.M.; Hilpakka, R.A.; Liao, S. Proc. Natl. Acad. Sci. U.S.A. 91, 10809-10813, 1994 A;Title: Ubiquitous receptor: a receptor that modulates A;Reference number: 159264; MUID:95062154 A;Accession: 159264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orphan nuclear receptor OR-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: (02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I59354; I59264 - withterm & C . Balto-Huikko M .: Gustafs
                                                                                                              A;Experimental source: vagina
C;Superfamily: unassigned erbA-related proteins; erbA transforming
C;Rupwords: DNA binding; zinc finger
F;76-366/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-32,'V',34-51,55-218,'V',220-446 <RE2>
A;Cross-references: EMBL:U14533; NID:g565661; PIDN:AAA52361.1; PID:g565662
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: IMBL:U20389; NID:g665941; PIDN:AAA69522.1; PID:g665942
                                                                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-446 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I59354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 APSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 ASSQGSGEGEGIQLTAAQELMIQQLVAAQLQCNKRSFS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 LCRLRKCKEAGMREQCVLSEEQIRKKR--IQKQQQQQPPPPSEPAASSSGRPAASPGTSE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ACRIRKCIESGMKKEMIMSDEAVEERRALIKRKKSER------TGTQP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 GPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GHELCRVCGDXASGFHYNVLSCEGCKGFFRRSVVHGGAGRYACRGSGTCQMDAFMRRKCQ 133
                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRL--LRIQDIHPFAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPSRVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHET---ECITFLKDFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFKGIISFAKYISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWEC----GRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLLSEIWDV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQ 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                         21.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LGAD-----PQSRDARQQRFA---HFTELAII 262
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Pred. No. 1.3e-30;
Score 487; DB 2;
Pred. No. 1.8e-30;
4; Mismatches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                  Length 446;
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     Indels
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       90;
                                                                                                                                                                        protein homology
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       Gaps
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37

GPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95

Matches 123;

Conservative

Best Local Similarity 28.68; Pred. No. 5.1e-28; Matches 130; Conservative 78; Mismatches 146; Indels 100; Gaps 16; Oy 5 PKESWNHADFVHCEDTESVPGRPSVNADEEVGGPQICRVCGDRATGYHFNVMTC 58	id x-activated receptor - rat s: Rattus norvegicus (Norway rat) 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 24 sion: A56918 1, B.M.; Goode, E.; Chen, J.; Oro, A.E.; Bradley, D.J.; Per 687-695, 1995 Identification of a nuclear receptor that is activated by nce number: A56918; MUID:95292336 sion: A56918 preliminary; nucleic acid sequence not shown le type: manA le type: manA le type: manA les: 1-469 <ford 0="" <erba="" amily:="" binding;="" dna="" domain:="" ds:="" erba="" erba-related="" finger="" gb:u18374;="" homology="" nid:9868031;="" nucleus;="" pid:98="" pidn:aac52205.1;="" protein="" proteins;="" references:="" transforming="" unassigned="" zinc=""></ford>	Qy 251 FKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVENAETGTWECGRLSY 306	74 96 134 139 194 191
		Search completed: February 18, 2001, 14:33:07 Job time: 5356 sec	Db 274

